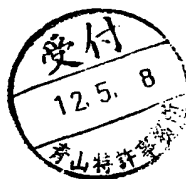


PATENT COOPERATION TREATY

From the:
INTERNATIONAL PRELIMINARY EXAMINING AUTHORITY

To:

AOYAMA, Tamotsu et al.
Aoyama & Partners
IMP Building, 3-7, Shiromi
1-chome, Chuo-ku, Osaka-shi
Osaka 540-0001
JAPON



PCT

WRITTEN OPINION

(PCT Rule 66)

Date of mailing (day/month/year)		02.05.2000	
Applicant's or agent's file reference 661102		REPLY DUE within 3 month(s) from the above date of mailing	
International application No. PCT/JP99/03929	International filing date (day/month/year) 22/07/1999	Priority date (day/month/year) 24/07/1998	
International Patent Classification (IPC) or both national classification and IPC C12N15/12			
Applicant SAGAMI CHEMICAL RESEARCH CENTER et al.			


1. This written opinion is the **first** drawn up by this International Preliminary Examining Authority.
2. This opinion contains indications relating to the following items:
 - I ☒ Basis of the opinion
 - II ☐ Priority
 - III ☒ Non-establishment of opinion with regard to novelty, inventive step and industrial applicability
 - IV ☐ Lack of unity of invention
 - V ☒ Reasoned statement under Rule 66.2(a)(ii) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement
 - VI ☐ Certain document cited
 - VII ☐ Certain defects in the international application
 - VIII ☐ Certain observations on the international application
3. The applicant is hereby **invited to reply** to this opinion.

When? See the time limit indicated above. The applicant may, before the expiration of that time limit, request this Authority to grant an extension, see Rule 66.2(d).

How? By submitting a written reply, accompanied, where appropriate, by amendments, according to Rule 66.3. For the form and the language of the amendments, see Rules 66.8 and 66.9.

Also: For an additional opportunity to submit amendments, see Rule 66.4.
For the examiner's obligation to consider amendments and/or arguments, see Rule 66.4 bis.
For an informal communication with the examiner, see Rule 66.6.

If no reply is filed, the international preliminary examination report will be established on the basis of this opinion.
4. The final date by which the international preliminary examination report must be established according to Rule 69.2 is: 24/11/2000.

Name and mailing address of the international preliminary examining authority:  European Patent Office D-80298 Munich Tel. +49 89 2399 - 0 Tx: 523656 epmu d Fax: +49 89 2399 - 4465	Authorized officer / Examiner Vollbach, S
	Formalities officer (incl. extension of time limits) Vullo, C Telephone No. +49 89 2399 8061



WRITTEN OPINION

International application No. PCT/JP99/03929

I. Basis of the opinion

1. This opinion has been drawn on the basis of *(substitute sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this opinion as "originally filed".)*:

Description, pages:

1-121 as originally filed

Claims, No.:

1-6 as originally filed

Drawings, sheets:

1/50-50/50 as originally filed

2. The amendments have resulted in the cancellation of:

- ☐ the description, pages:
- ☐ the claims, Nos.:
- ☐ the drawings, sheets:

3. This opinion has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed (Rule 70.2(c)):

4. Additional observations, if necessary:

III. Non-establishment of opinion with regard to novelty, inventive step and industrial applicability

The questions whether the claimed invention appears to be novel, to involve an inventive step (to be non-obvious), or to be industrially applicable have not been and will not be examined in respect of:

- ☐ the entire international application,
- ☒ claims Nos. 1-6 partially,

because:

- ☐ the said international application, or the said claims Nos. relate to the following subject matter which does not require an international preliminary examination (*specify*):

WRITTEN OPINION

International application No. PCT/JP99/03929

- ☐ the description, claims or drawings (*indicate particular elements below*) or said claims Nos. are so unclear that no meaningful opinion could be formed (*specify*):
- ☐ the claims, or said claims Nos. are so inadequately supported by the description that no meaningful opinion could be formed.
- ☒ no international search report has been established for the said claims Nos. 1-6 partially.

V. Reasoned statement under Rule 66.2(a)(ii) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. Statement

Novelty (N)	Claims
Inventive step (IS)	Claims 1-6
Industrial applicability (IA)	Claims

2. Citations and explanations

see separate sheet

1. The search authority raised an objection for lack of unity of the application. Since no required additional search fees were paid by the applicant, search has only been carried out on the invention first mentioned in the claims i.e. Seq. ID Nos 1,11 and 21. Examination can thus only be based on said subject-matter.

2. The present application relates to a protein having the amino acid sequence shown in Seq ID No 1, the cDNA shown in Seq. ID Nos 11 and 21, expression vectors comprising these sequences and transformed eucaryotic hosts.

The DNA sequences have been selected from cDNA libraries by the presence of a hydrophobic region being a putative secretory signal or transmembrane.

In particular the clone HP01550 (Seq. ID Nos 1,11, and 21) is a clone from a human stomach cancer cDNA library which consists of 65-bp 5'-untranslated region, a 378-bp ORF, and a 67-bp 3' untranslated region. The ORF codes for a protein of 125 amino acids and the expressed protein has a molecular weight of 15 kDa. Search in a protein data base revealed a similarity to the *Caenorhabditis elegans* hypothetical proteins F45G2.c and F45G2.c. In addition the search of the GenBank revealed an EST which shares more than 90% homology.

3. As far as patentability of the specific claimed sequences are concerned the following considerations apply:

The specific claimed sequences are new according to the requirements set out in Article 33(2) PCT.

However, an inventive step cannot be recognized because in general the provision of a DNA sequence without an indication of how to use said DNA sequence (specific technical purpose) is not inventive per se (Article 33(3) PCT). This also apply to the encoded protein even if expression has been carried out.

It should be noted, that all subject-matter which might involve a certain contribution to the art, namely the determination of the function of the protein and methods which make use of said protein and the encoding DNA sequence have not been carried out. Therefore an inventive step is not recognized by the present authority for claims 1-6 (Article 33(3) PCT).

PATENT COOPERATION TREATY

PCT

NOTIFICATION OF RECEIPT OF
RECORD COPY

(PCT Rule 24.2(a))



From the INTERNATIONAL BUREAU

To:

AOYAMA, Tamotsu
 AOYAMA & PARTNERS
 IMP Building
 3-7, Shiromi 1-chome, Chuo-ku
 Osaka-shi
 Osaka 540-0001
 JAPON

Date of mailing (day/month/year) 17 August 1999 (17.08.99)	IMPORTANT NOTIFICATION
Applicant's or agent's file reference 661102	International application No. PCT/JP99/03929

The applicant is hereby notified that the International Bureau has received the record copy of the international application as detailed below.

Name(s) of the applicant(s) and State(s) for which they are applicants:

SAGAMI CHEMICAL RESEARCH CENTER et al (for all designated States except US)
 KATO, Seishi et al (for US)

International filing date	:	22 July 1999 (22.07.99)
Priority date(s) claimed	:	24 July 1998 (24.07.98) 07 August 1998 (07.08.98) 25 August 1998 (25.08.98) 09 September 1998 (09.09.98) 29 September 1998 (29.09.98)

Date of receipt of the record copy by the International Bureau	:	06 August 1999 (06.08.99)
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List of designated Offices :

AP : GH, GM, KE, LS, MW, SD, SZ, UG, ZW
 EA : AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
 EP : AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
 OA : BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
 National : AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE,
 GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO,
 NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW

The International Bureau of WIPO 34, chemin des Colombettes 1211 Geneva 20, Switzerland	Authorized officer: M. Sakai
Facsimile No. (41-22) 740.14.35	Telephone No. (41-22) 338.83.38

Continuation of Form PCT/IB/3

NOTIFICATION OF RECEIPT OF RECORD COPY

Date of mailing (day/month/year) 17 August 1999 (17.08.99)	IMPORTANT NOTIFICATION
Applicant's or agent's file reference 661102	International application No. PCT/JP99/03929

ATTENTION

The applicant should carefully check the data appearing in this Notification. In case of any discrepancy between these data and the indications in the international application, the applicant should immediately inform the International Bureau.

In addition, the applicant's attention is drawn to the information contained in the Annex, relating to:

- ☒ time limits for entry into the national phase
- ☒ confirmation of precautionary designations
- ☒ requirements regarding priority documents

A copy of this Notification is being sent to the receiving Office and to the International Searching Authority.

INFORMATION ON TIME LIMITS FOR ENTERING THE NATIONAL PHASE

The applicant is reminded that the "national phase" must be entered before each of the designated Offices indicated in the Notification of Receipt of Record Copy (Form PCT/IB/301) by paying national fees and furnishing translations, as prescribed by the applicable national laws.

The time limit for performing these procedural acts is **20 MONTHS** from the priority date or, for those designated States which the applicant elects in a demand for international preliminary examination or in a later election, **30 MONTHS** from the priority date, provided that the election is made before the expiration of 19 months from the priority date. Some designated (or elected) Offices have fixed time limits which expire even later than 20 or 30 months from the priority date. In other Offices an extension of time or grace period, in some cases upon payment of an additional fee, is available.

In addition to these procedural acts, the applicant may also have to comply with other special requirements applicable in certain Offices. It is the applicant's responsibility to ensure that the necessary steps to enter the national phase are taken in a timely fashion. Most designated Offices do not issue reminders to applicants in connection with the entry into the national phase.

For detailed information about the procedural acts to be performed to enter the national phase before each designated Office, the applicable time limits and possible extensions of time or grace periods, and any other requirements, see the relevant Chapters of Volume II of the PCT Applicant's Guide. Information about the requirements for filing a demand for international preliminary examination is set out in Chapter IX of Volume I of the PCT Applicant's Guide.

GR and ES became bound by PCT Chapter II on 7 September 1996 and 6 September 1997, respectively, and may, therefore, be elected in a demand or a later election filed on or after 7 September 1996 and 6 September 1997, respectively, regardless of the filing date of the international application. (See second paragraph above.)

Note that only an applicant who is a national or resident of a PCT Contracting State which is bound by Chapter II has the right to file a demand for international preliminary examination.

CONFIRMATION OF PRECAUTIONARY DESIGNATIONS

This notification lists only specific designations made under Rule 4.9(a) in the request. It is important to check that these designations are correct. Errors in designations can be corrected where precautionary designations have been made under Rule 4.9(b). The applicant is hereby reminded that any precautionary designations may be confirmed according to Rule 4.9(c) before the expiration of 15 months from the priority date. If it is not confirmed, it will automatically be regarded as withdrawn by the applicant. There will be no reminder and no invitation. Confirmation of a designation consists of the filing of a notice specifying the designated State concerned (with an indication of the kind of protection or treatment desired) and the payment of the designation and confirmation fees. Confirmation must reach the receiving Office within the 15-month time limit.

REQUIREMENTS REGARDING PRIORITY DOCUMENTS

For applicants who have not yet complied with the requirements regarding priority documents, the following is recalled.

Where the priority of an earlier national, regional or international application is claimed, the applicant must submit a copy of the said earlier application, certified by the authority with which it was filed ("the priority document") to the receiving Office (which will transmit it to the International Bureau) or directly to the International Bureau, before the expiration of 16 months from the priority date, provided that any such priority document may still be submitted to the International Bureau before that date of international publication of the international application, in which case that document will be considered to have been received by the International Bureau on the last day of the 16-month time limit (Rule 17.1(a)).

Where the priority document is issued by the receiving Office, the applicant may, instead of submitting the priority document, request the receiving Office to prepare and transmit the priority document to the International Bureau. Such request must be made before the expiration of the 16-month time limit and may be subjected by the receiving Office to the payment of a fee (Rule 17.1(b)).

If the priority document concerned is not submitted to the International Bureau or if the request to the receiving Office to prepare and transmit the priority document has not been made (and the corresponding fee, if any, paid) within the applicable time limit indicated under the preceding paragraphs, any designated State may disregard the priority claim, provided that no designated Office may disregard the priority claim concerned before giving the applicant an opportunity to furnish the priority document within a time limit which is reasonable under the circumstances.

Where several priorities are claimed, the priority date to be considered for the purposes of computing the 16-month time limit is the filing date of the earliest application whose priority is claimed.

PATENT COOPERATION TREATY

PCT

NOTIFICATION CONCERNING
SUBMISSION OR TRANSMITTAL
OF PRIORITY DOCUMENT

(PCT Administrative Instructions, Section 411)

From the INTERNATIONAL BUREAU

To:

AOYAMA, Tamotsu
AOYAMA & PARTNERS
IMP Building
3-7, Shiromi 1-chome, Chuo-ku
Osaka-shi
Osaka 540-0001
JAPON

Date of mailing (day/month/year)
06 October 1999 (06.10.99)

Applicant's or agent's file reference
661102

International application No.
PCT/JP99/03929

International publication date (day/month/year)
Not yet published

International filing date (day/month/year)
22 July 1999 (22.07.99)

Priority date (day/month/year)
24 July 1998 (24.07.98)

Applicant

SAGAMI CHEMICAL RESEARCH CENTER et al

IMPORTANT NOTIFICATION

1. The applicant is hereby notified of the date of receipt (except where the letters "NR" appear in the right-hand column) by the International Bureau of the priority document(s) relating to the earlier application(s) indicated below. Unless otherwise indicated by an asterisk appearing next to a date of receipt, or by the letters "NR", in the right-hand column, the priority document concerned was submitted or transmitted to the International Bureau in compliance with Rule 17.1(a) or (b).
2. This updates and replaces any previously issued notification concerning submission or transmittal of priority documents.
3. An asterisk(*) appearing next to a date of receipt, in the right-hand column, denotes a priority document submitted or transmitted to the International Bureau but not in compliance with Rule 17.1(a) or (b). In such a case, the attention of the applicant is directed to Rule 17.1(c) which provides that no designated Office may disregard the priority claim concerned before giving the applicant an opportunity, upon entry into the national phase, to furnish the priority document within a time limit which is reasonable under the circumstances.
4. The letters "NR" appearing in the right-hand column denote a priority document which was not received by the International Bureau or which the applicant did not request the receiving Office to prepare and transmit to the International Bureau, as provided by Rule 17.1(a) or (b), respectively. In such a case, the attention of the applicant is directed to Rule 17.1(c) which provides that no designated Office may disregard the priority claim concerned before giving the applicant an opportunity, upon entry into the national phase, to furnish the priority document within a time limit which is reasonable under the circumstances.

<u>Priority date</u>	<u>Priority application No.</u>	<u>Country or regional Office or PCT receiving Office</u>	<u>Date of receipt of priority document</u>
24 July 1998 (24.07.98)	10/208820	JP	27 Sept 1999 (27.09.99)

The International Bureau of WIPO
34, chemin des Colombettes
1211 Geneva 20, Switzerland

Facsimile No. (41-22) 740.14.35

Authorized officer

Juan Cruz

Telephone No. (41-22) 338.83.38

Form PCT/IB/304 (July 1998)

002881955

外国方式

PATENT COOPERATION TREATY

WO 00/05367
PCT/JP99/03929

PCT

NOTICE INFORMING THE APPLICANT OF THE COMMUNICATION OF THE INTERNATIONAL APPLICATION TO THE DESIGNATED OFFICES

(PCT Rule 47.1(c), first sentence)

From the INTERNATIONAL BUREAU

To:

AOYAMA, Tamotsu
Aoyama & Partners
IMP Building
3-7, Shiromi 1-chome, Chuo-ku
Osaka-shi
Osaka 540-0001
JAPON



Date of mailing (day/month/year) 03 February 2000 (03.02.00)		
Applicant's or agent's file reference 661102		IMPORTANT NOTICE
International application No. PCT/JP99/03929	International filing date (day/month/year) 22 July 1999 (22.07.99)	Priority date (day/month/year) 24 July 1998 (24.07.98)
Applicant SAGAMI CHEMICAL RESEARCH CENTER et al		

1. Notice is hereby given that the International Bureau has communicated, as provided in Article 20, the international application to the following designated Offices on the date indicated above as the date of mailing of this Notice:
AU,CN,EP,IL,JP,KR,US

In accordance with Rule 47.1(c), third sentence, those Offices will accept the present Notice as conclusive evidence that the communication of the international application has duly taken place on the date of mailing indicated above and no copy of the international application is required to be furnished by the applicant to the designated Office(s).

2. The following designated Offices have waived the requirement for such a communication at this time:
AE,AL,AM,AP,AT,AZ,BA,BB,BG,BR,BY,CA,CH,CU,CZ,DE,DK,EA,EE,ES,FI,GB,GD,GE,GH,GM,HR,
HU,ID,IN,IS,KE,KG,KZ,LC,LK,LR,LS,LT,LU,LV,MD,MG,MK,MN,MW,MX,NO,NZ,OA,PL,PT,RO,RU,
SD,SE,SG,SI,SK,SL,TJ,TM,TR,TT,UA,UG,UZ,VN,YU,ZA,ZW
The communication will be made to those Offices only upon their request. Furthermore, those Offices do not require the applicant to furnish a copy of the international application (Rule 49.1(a-bis)).
3. Enclosed with this Notice is a copy of the international application as published by the International Bureau on
03 February 2000 (03.02.00) under No. WO 00/05367

REMINDER REGARDING CHAPTER II (Article 31(2)(a) and Rule 54.2)

If the applicant wishes to postpone entry into the national phase until 30 months (or later in some Offices) from the priority date, a demand for international preliminary examination must be filed with the competent International Preliminary Examining Authority before the expiration of 19 months from the priority date.

It is the applicant's sole responsibility to monitor the 19-month time limit.

Note that only an applicant who is a national or resident of a PCT Contracting State which is bound by Chapter II has the right to file a demand for international preliminary examination.

REMINDER REGARDING ENTRY INTO THE NATIONAL PHASE (Article 22 or 39(1))

If the applicant wishes to proceed with the international application in the national phase, he must, within 20 months or 30 months, or later in some Offices, perform the acts referred to therein before each designated or elected Office.

For further important information on the time limits and acts to be performed for entering the national phase, see the Annex to Form PCT/IB/301 (Notification of Receipt of Record Copy) and Volume II of the PCT Applicant's Guide.

The International Bureau of WIPO 34, chemin des Colombettes 1211 Geneva 20, Switzerland	Authorized officer J. Zahra
Facsimile No. (41-22) 740.14.35	Telephone No. (41-22) 338.83.38

PATENT COOPERATION TREATY

PCT

INFORMATION CONCERNING ELECTED
OFFICES NOTIFIED OF THEIR ELECTION

(PCT Rule 61.3)

From the INTERNATIONAL BUREAU

To:

AOYAMA, Tamotsu
Aoyama & Partners
IMP Building
3-7, Shiromi 1-chome, Chuo-ku
Osaka-shi
Osaka 540-0001
JAPON

Date of mailing (day/month/year)
01 March 2000 (01.03.00)

Applicant's or agent's file reference
661102

IMPORTANT INFORMATION

International application No.
PCT/JP99/03929

International filing date (day/month/year)
22 July 1999 (22.07.99)

Priority date (day/month/year)
24 July 1998 (24.07.98)

Applicant

SAGAMI CHEMICAL RESEARCH CENTER et al

1. The applicant is hereby informed that the International Bureau has, according to Article 31(7), notified each of the following Offices of its election:

AP : GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW

EP : AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

National : AU, BG, BR, CA, CN, CZ, DE, IL, JP, KR, MN, NO, NZ, PL, RO, RU, SE, SK, US

2. The following Offices have waived the requirement for the notification of their election; the notification will be sent to them by the International Bureau only upon their request:

EA : AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

OA : BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

National : AE, AL, AM, AT, AZ, BA, BB, BY, CH, CU, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU,
ID, IN, IS, KE, KG, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MW, MX, PT, SD, SG, SI, SL, TJ,
TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW

3. The applicant is reminded that he must enter the "national phase" before the expiration of 30 months from the priority date before each of the Offices listed above. This must be done by paying the national fee(s) and furnishing, if prescribed, a translation of the international application (Article 39(1)(a)), as well as, where applicable, by furnishing a translation of any annexes of the international preliminary examination report (Article 36(3)(b) and Rule 74.1).

Some offices have fixed time limits expiring later than the above-mentioned time limit. For detailed information about the applicable time limits and the acts to be performed upon entry into the national phase before a particular Office, see Volume II of the PCT Applicant's Guide.

The entry into the European regional phase is postponed until 31 months from the priority date for all States designated for the purposes of obtaining a European patent.

The International Bureau of WIPO
34, chemin des Colombettes
1211 Geneva 20, Switzerland

Facsimile No. (41-22) 740.14.35

Authorized officer:

R. Forax

Telephone No. (41-22) 338.83.38

3136756

From the
INTERNATIONAL PRELIMINARY EXAMINING AUTHORITY

PCT

To:

AOYAMA, Tamotsu et al.
Aoyama & Partners
IMP Building, 3-7, Shiromi
1-chome, Chuo-ku, Osaka-shi
Osaka 540-0001
JAPON



**NOTIFICATION OF RECEIPT
OF DEMAND BY COMPETENT INTERNATIONAL
PRELIMINARY EXAMINING AUTHORITY**

(PCT Rules 59.3(e) and 61.1(b), first sentence
and Administrative Instructions, Section 601(a))

Date of mailing
(day/month/year)

18. 02. 00

Applicant's or agent's file reference
661102

IMPORTANT NOTIFICATION

International application No.

PCT/ JP 99/ 03929

International filing date (day/month/year)

22/07/1999

Priority date (day/month/year)

24/07/1998

Applicant

SAGAMI CHEMICAL RESEARCH CENTER et al.

1. The applicant is hereby notified that this International Preliminary Examining Authority considers the following date as the date of receipt of the demand for international preliminary examination of the international application:

03/02/2000

2. This date of receipt is:



the actual date of receipt of the demand by this Authority (Rule 61.1(b)).



the actual date of receipt of the demand on behalf of this Authority (Rule 59.3(e)).



the date on which this Authority has, in response to the invitation to correct defects in the demand (Form PCT/IPEA/404), received the required corrections.

3. ☐ **ATTENTION:** That date of receipt is **AFTER** the expiration of 19 months from the priority date. Consequently, the election(s) made in the demand does (do) not have the effect of postponing the entry into the national phase until 30 months from the priority date (or later in some Offices) (Article 39(1)). Therefore, the acts for entry into the national phase must be performed within 20 months from the priority date (or later in some Offices) (Article 22). For details, see the *PCT Applicant's Guide*, Volume II.



(If applicable) This notification confirms the information given by telephone, facsimile transmission or in person on:

4. Only where paragraph 3 applies, a copy of this notification has been sent to the International Bureau.

Name and mailing address of the IPEA/



European Patent Office
D-80298 Munich
Tel. (+49-89) 2399-0, Tx: 523656 epmu d
Fax: (+49-89) 2399-4465

Authorized officer

DANISSEN P T

Tel. (+49-89) 2399-8862



REC'D 15 NOV 2000

WIPO PCT

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Article 36 and Rule 70)

Applicant's or agent's file reference 661102	FOR FURTHER ACTION See Notification of Transmittal of International Preliminary Examination Report (Form PCT/IPEA/416)	
International application No. PCT/JP99/03929	International filing date (day/month/year) 22/07/1999	Priority date (day/month/year) 24/07/1998
International Patent Classification (IPC) or national classification and IPC C12N15/12		
Applicant SAGAMI CHEMICAL RESEARCH CENTER et al.		

1. This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36.



2. This REPORT consists of a total of 5 sheets, including this cover sheet.

- ☐ This report is also accompanied by ANNEXES, i.e. sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT).

These annexes consist of a total of sheets.

3. This report contains indications relating to the following items:

- I ☒ Basis of the report
- II ☐ Priority
- III ☒ Non-establishment of opinion with regard to novelty, inventive step and industrial applicability
- IV ☐ Lack of unity of invention
- V ☒ Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement
- VI ☐ Certain documents cited
- VII ☐ Certain defects in the international application
- VIII ☐ Certain observations on the international application

Date of submission of the demand 03/02/2000	Date of completion of this report 13.11.2000
Name and mailing address of the international preliminary examining authority:  European Patent Office D-80298 Munich Tel. +49 89 2399 - 0 Tx: 523656 epmu d Fax: +49 89 2399 - 4465	Authorized officer Vollbach, S Telephone No. +49 89 2399 8715 

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No. PCT/JP99/03929

I. Basis of the report

1. This report has been drawn on the basis of *(substitute sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to the report since they do not contain amendments (Rules 70.16 and 70.17).):*

Description, pages:

1-121 as originally filed

Claims, No.:

1-6 as originally filed

Drawings, sheets:

1/50-50/50 as originally filed

2. With regard to the **language**, all the elements marked above were available or furnished to this Authority in the language in which the international application was filed, unless otherwise indicated under this item.

These elements were available or furnished to this Authority in the following language: , which is:

- ☐ the language of a translation furnished for the purposes of the international search (under Rule 23.1(b)).
- ☐ the language of publication of the international application (under Rule 48.3(b)).
- ☐ the language of a translation furnished for the purposes of international preliminary examination (under Rule 55.2 and/or 55.3).

3. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international preliminary examination was carried out on the basis of the sequence listing:

- ☐ contained in the international application in written form.
- ☐ filed together with the international application in computer readable form.
- ☐ furnished subsequently to this Authority in written form.
- ☐ furnished subsequently to this Authority in computer readable form.
- ☐ The statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.
- ☐ The statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished.

4. The amendments have resulted in the cancellation of:

- ☐ the description, pages:
- ☐ the claims, Nos.:

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No. PCT/JP99/03929

☐ the drawings, sheets:

5. ☐ This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed (Rule 70.2(c)):

(Any replacement sheet containing such amendments must be referred to under item 1 and annexed to this report.)

6. Additional observations, if necessary:

III. Non-establishment of opinion with regard to novelty, inventive step and industrial applicability

The questions whether the claimed invention appears to be novel, to involve an inventive step (to be non-obvious), or to be industrially applicable have not been examined in respect of:

☐ the entire international application.

☒ claims Nos. 1-6 partially.

because:

☐ the said international application, or the said claims Nos. relate to the following subject matter which does not require an international preliminary examination (*specify*):

☐ the description, claims or drawings (*indicate particular elements below*) or said claims Nos. are so unclear that no meaningful opinion could be formed (*specify*):

☐ the claims, or said claims Nos. are so inadequately supported by the description that no meaningful opinion could be formed.

☒ no international search report has been established for the said claims Nos. 1-6 partially.

2. A meaningful international preliminary examination report cannot be carried out due to the failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions:

☐ the written form has not been furnished or does not comply with the standard.

☐ the computer readable form has not been furnished or does not comply with the standard.

V. Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. Statement

Novelty (N)

Yes: Claims 1-6

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No. PCT/JP99/03929

	No:	Claims	
Inventive step (IS)	Yes:	Claims	
	No:	Claims	1-6
Industrial applicability (IA)	Yes:	Claims	
	No:	Claims	1-6

2. Citations and explanations
see separate sheet

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT - SEPARATE SHEET**

International application No. PCT/JP99/03929

1. The search authority raised an objection for lack of unity of the application. Since no required additional search fees were paid by the applicant, search has only been carried out on the invention first mentioned in the claims i.e. Seq. ID Nos 1,11 and 21. Examination can thus only be based on said subject-matter.

2. The present application relates to a protein having the amino acid sequence shown in Seq ID No 1, the cDNA shown in Seq. ID Nos 11 and 21, expression vectors comprising these sequences and transformed eucaryotic hosts.

The DNA sequences have been selected from cDNA libraries by the presence of a hydrophobic region being a putative secretory signal or transmembrane.

In particular the clone HP01550 (Seq. ID Nos 1,11, and 21) is a clone from a human stomach cancer cDNA library which consists of 65-bp 5'-untranslated region, a 378-bp ORF, and a 67-bp 3' untranslated region. The ORF codes for a protein of 125 amino acids and the expressed protein has a molecular weight of 15 kDa. Search in a protein data base revealed a similarity to the *Caenorhabditis elegans* hypothetical proteins F45G2.c and F45G2.c. In addition the search of the GenBank revealed an EST which shares more than 90% homology.

3. As far as patentability of the specific claimed sequences are concerned the following considerations apply:

The specific claimed sequences are new according to the requirements set out in Article 33(2) PCT.

However, an inventive step cannot be recognized because in general the provision of a DNA sequence without an indication of how to use said DNA sequence (specific technical purpose) is not inventive per se (Article 33(3) PCT) and cannot be regarded as industrial applicable. This also apply to the encoded protein even if expression has been carried out.

It should be noted, that any subject-matter which might involve a certain contribution to the art, namely the determination of the function of the protein and methods which make use of said protein and the encoding DNA sequence have not been carried out. Therefore an inventive step is not recognized by the present authority for claims 1-6 (Article 33(3) PCT).

From the
INTERNATIONAL PRELIMINARY EXAMINING AUTHORITY

To:

AOYAMA, Tamotsu et al.
Aoyama & Partners
IMP Building, 3-7, Shiromi
1-chome, Chuo-ku, Osaka-shi
Osaka 540-0001
JAPON



PCT

NOTIFICATION OF TRANSMITTAL OF
THE INTERNATIONAL PRELIMINARY
EXAMINATION REPORT
(PCT Rule 71.1)

Date of mailing
(day/month/year) 13.11.2000

Applicant's or agent's file reference
661102

IMPORTANT NOTIFICATION

International application No.
PCT/JP99/03929

International filing date (day/month/year)
22/07/1999

Priority date (day/month/year)
24/07/1998

Applicant
SAGAMI CHEMICAL RESEARCH CENTER et al.

1. The applicant is hereby notified that this International Preliminary Examining Authority transmits herewith the international preliminary examination report and its annexes, if any, established on the international application.
2. A copy of the report and its annexes, if any, is being transmitted to the International Bureau for communication to all the elected Offices.
3. Where required by any of the elected Offices, the International Bureau will prepare an English translation of the report (but not of any annexes) and will transmit such translation to those Offices.

4. REMINDER

The applicant must enter the national phase before each elected Office by performing certain acts (filing translations and paying national fees) within 30 months from the priority date (or later in some Offices) (Article 39(1)) (see also the reminder sent by the International Bureau with Form PCT/IB/301).

Where a translation of the international application must be furnished to an elected Office, that translation must contain a translation of any annexes to the international preliminary examination report. It is the applicant's responsibility to prepare and furnish such translation directly to each elected Office concerned.

For further details on the applicable time limits and requirements of the elected Offices, see Volume II of the PCT Applicant's Guide.

Name and mailing address of the IPEA/

 European Patent Office
D-80298 Munich
Tel. +49 89 2399 - 0 Tx: 523656 epmu d
Fax: +49 89 2399 - 4465

Authorized officer

Emslander, S

Tel. +49 89 2399-8718





PATENT COOPERATION TREATY

PCT

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Article 36 and Rule 70)

Applicant's or agent's file reference 661102		See Notification of Transmittal of International Preliminary Examination Report (Form PCT/IPEA/416) FOR FURTHER ACTION	
International application No. PCT/JP99/03929	International filing date (day/month/year) 22/07/1999	Priority date (day/month/year) 24/07/1998	
International Patent Classification (IPC) or national classification and IPC C12N15/12			
Applicant SAGAMI CHEMICAL RESEARCH CENTER et al.			
<p>1. This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36.</p> <p>2. This REPORT consists of a total of 5 sheets, including this cover sheet.</p> <p><input type="checkbox"/> This report is also accompanied by ANNEXES, i.e. sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT).</p> <p>These annexes consist of a total of sheets.</p>			
<p>3. This report contains indications relating to the following items:</p> <ul style="list-style-type: none"> I <input checked="" type="checkbox"/> Basis of the report II <input type="checkbox"/> Priority III <input checked="" type="checkbox"/> Non-establishment of opinion with regard to novelty, inventive step and industrial applicability IV <input type="checkbox"/> Lack of unity of invention V <input checked="" type="checkbox"/> Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement VI <input type="checkbox"/> Certain documents cited VII <input type="checkbox"/> Certain defects in the international application VIII <input type="checkbox"/> Certain observations on the international application 			
Date of submission of the demand 03/02/2000		Date of completion of this report 13.11.2000	
Name and mailing address of the international preliminary examining authority:  European Patent Office D-80298 Munich Tel. +49 89 2399 - 0 Tx: 523656 epmu d Fax: +49 89 2399 - 4465		Authorized officer Vollbach, S Telephone No. +49 89 2399 8715 	

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT**

International application No. PCT/JP99/03929

I. Basis of the report

1. This report has been drawn on the basis of *(substitute sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to the report since they do not contain amendments (Rules 70.16 and 70.17).)*:

Description, pages:

1-121 as originally filed

Claims, No.:

1-6 as originally filed

Drawings, sheets:

1/50-50/50 as originally filed

2. With regard to the **language**, all the elements marked above were available or furnished to this Authority in the language in which the international application was filed, unless otherwise indicated under this item.

These elements were available or furnished to this Authority in the following language: , which is:

- ☐ the language of a translation furnished for the purposes of the international search (under Rule 23.1(b)).
- ☐ the language of publication of the international application (under Rule 48.3(b)).
- ☐ the language of a translation furnished for the purposes of international preliminary examination (under Rule 55.2 and/or 55.3).

3. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international preliminary examination was carried out on the basis of the sequence listing:

- ☐ contained in the international application in written form.
- ☐ filed together with the international application in computer readable form.
- ☐ furnished subsequently to this Authority in written form.
- ☐ furnished subsequently to this Authority in computer readable form.
- ☐ The statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.
- ☐ The statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished.

4. The amendments have resulted in the cancellation of:

- ☐ the description, pages:
- ☐ the claims, Nos.:

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT**

International application No. PCT/JP99/03929

☐ the drawings, sheets:

5. ☐ This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed (Rule 70.2(c)):

(Any replacement sheet containing such amendments must be referred to under item 1 and annexed to this report.)

6. Additional observations, if necessary:

III. Non-establishment of opinion with regard to novelty, inventive step and industrial applicability

The questions whether the claimed invention appears to be novel, to involve an inventive step (to be non-obvious), or to be industrially applicable have not been examined in respect of:

☐ the entire international application.

☒ claims Nos. 1-6 partially.

because:

☐ the said international application, or the said claims Nos. relate to the following subject matter which does not require an international preliminary examination (*specify*):

☐ the description, claims or drawings (*indicate particular elements below*) or said claims Nos. are so unclear that no meaningful opinion could be formed (*specify*):

☐ the claims, or said claims Nos. are so inadequately supported by the description that no meaningful opinion could be formed.

☒ no international search report has been established for the said claims Nos. 1-6 partially.

2. A meaningful international preliminary examination report cannot be carried out due to the failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions:

☐ the written form has not been furnished or does not comply with the standard.

☐ the computer readable form has not been furnished or does not comply with the standard.

V. Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. Statement

Novelty (N)

Yes: Claims 1-6

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT**

International application No. PCT/JP99/03929

	No:	Claims	
Inventive step (IS)	Yes:	Claims	
	No:	Claims	1-6
Industrial applicability (IA)	Yes:	Claims	
	No:	Claims	1-6

2. Citations and explanations
see separate sheet

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT - SEPARATE SHEET**

International application No. PCT/JP99/03929

1. The search authority raised an objection for lack of unity of the application. Since no required additional search fees were paid by the applicant, search has only been carried out on the invention first mentioned in the claims i.e. Seq. ID Nos 1,11 and 21. Examination can thus only be based on said subject-matter.

2. The present application relates to a protein having the amino acid sequence shown in Seq ID No 1, the cDNA shown in Seq. ID Nos 11 and 21, expression vectors comprising these sequences and transformed eucaryotic hosts.

The DNA sequences have been selected from cDNA libraries by the presence of a hydrophobic region being a putative secretory signal or transmembrane.

In particular the clone HP01550 (Seq. ID Nos 1,11, and 21) is a clone from a human stomach cancer cDNA library which consists of 65-bp 5'-untranslated region, a 378-bp ORF, and a 67-bp 3' untranslated region. The ORF codes for a protein of 125 amino acids and the expressed protein has a molecular weight of 15 kDa. Search in a protein data base revealed a similarity to the *Caenorhabditis elegans* hypothetical proteins F45G2.c and F45G2.c. In addition the search of the GenBank revealed an EST which shares more than 90% homology.

3. As far as patentability of the specific claimed sequences are concerned the following considerations apply:

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It should be noted, that any subject-matter which might involve a certain contribution to the art, namely the determination of the function of the protein and methods which make use of said protein and the encoding DNA sequence have not been carried out. Therefore an inventive step is not recognized by the present authority for claims 1-6 (Article 33(3) PCT).

PCT REQUEST

Original (for SUBMISSION) - printed on 16.07.1999 10:35:27 AM

0	For receiving Office use only	
0-1	International Application No.	
0-2	International Filing Date	
0-3	Name of receiving Office and "PCT International Application"	

0-4	Form - PCT/RO/101 PCT Request	
0-4-1	Prepared using	PCT-EASY Version 2.84 (updated 01.07.1999)
0-5	Petition The undersigned requests that the present international application be processed according to the Patent Cooperation Treaty	
0-6	Receiving Office (specified by the applicant)	Japanese Patent Office (RO/JP)
0-7	Applicant's or agent's file reference	661102
I	Title of invention	HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE PROTEINS
II	Applicant	
II-1	This person is:	applicant only
II-2	Applicant for	all designated States except US
II-4	Name	SAGAMI CHEMICAL RESEARCH CENTER
II-5	Address:	4-1, Nishi-Ohnuma 4-chome, Sagamihara-shi, Kanagawa 229-0012 Japan
II-6	State of nationality	JP
II-7	State of residence	JP
III-1	Applicant and/or inventor	
III-1-1	This person is:	applicant only
III-1-2	Applicant for	all designated States except US
III-1-4	Name	PROTEGENE INC.
III-1-5	Address:	2-20-3, Naka-cho, Meguro-ku, Tokyo 153-0065 Japan
III-1-6	State of nationality	JP
III-1-7	State of residence	JP

PCT REQUEST

Original (for SUBMISSION) - printed on 16.07.1999 10:35:27 AM

III-2	Applicant and/or inventor	applicant and inventor US only KATO, Seishi 3-46-50, Wakamatsu, Sagamihara-shi, Kanagawa 229-0014 Japan JP JP
III-2-1	This person is:	
III-2-2	Applicant for	
III-2-4	Name (LAST, First)	
III-2-5	Address:	
III-2-6	State of nationality	
III-2-7	State of residence	
III-3	Applicant and/or inventor	applicant and inventor US only KIMURA, Tomoko 302, 4-1-28, Nishiikuta, Tama-ku, Kawasaki-shi, Kanagawa 214-0037 Japan JP JP
III-3-1	This person is:	
III-3-2	Applicant for	
III-3-4	Name (LAST, First)	
III-3-5	Address:	
III-3-6	State of nationality	
III-3-7	State of residence	
IV-1	Agent or common representative; or address for correspondence The person identified below is hereby/has been appointed to act on behalf of the applicant(s) before the competent International Authorities as:	agent AOYAMA, Tamotsu AOYAMA & PARTNERS IMP Building, 3-7, Shiromi 1-chome, chuo-ku, Osaka-shi, Osaka 540-0001 Japan (06) 6949-1261 (06) 6949-0361
IV-1-1	Name (LAST, First)	
IV-1-2	Address:	
IV-1-3	Telephone No.	
IV-1-4	Facsimile No.	
IV-2	Additional agent(s)	
IV-2-1	Name(s)	additional agent(s) with same address as first named agent TAMURA, Yasuo; IWASAKI, Mitsutaka

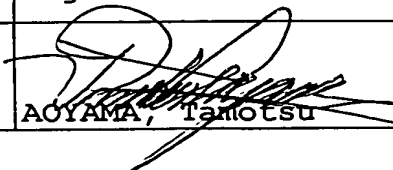
PCT REQUEST

Original (for SUBMISSION) - printed on 16.07.1999 10:35:27 AM

V	Designation of States	
V-1	Regional Patent (other kinds of protection or treatment, if any, are specified between parentheses after the designation(s) concerned)	<p>AP: GH GM KE LS MW SD SZ UG ZW and any other State which is a Contracting State of the Harare Protocol and of the PCT</p> <p>EA: AM AZ BY KG KZ MD RU TJ TM and any other State which is a Contracting State of the Eurasian Patent Convention and of the PCT</p> <p>EP: AT BE CH&LI CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE and any other State which is a Contracting State of the European Patent Convention and of the PCT</p> <p>OA: BF BJ CF CG CI CM GA GN GW ML MR NE SN TD TG and any other State which is a member State of OAPI and a Contracting State of the PCT</p>
V-2	National Patent (other kinds of protection or treatment, if any, are specified between parentheses after the designation(s) concerned)	<p>AE AL AM AT AU AZ BA BB BG BR BY CA CH&LI CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZA ZW</p>
V-5	Precautionary Designation Statement In addition to the designations made under items V-1, V-2 and V-3, the applicant also makes under Rule 4.9(b) all designations which would be permitted under the PCT except any designation(s) of the State(s) indicated under item V-6 below. The applicant declares that those additional designations are subject to confirmation and that any designation which is not confirmed before the expiration of 15 months from the priority date is to be regarded as withdrawn by the applicant at the expiration of that time limit.	
V-6	Exclusion(s) from precautionary designations	NONE
VI-1	Priority claim of earlier national application	
VI-1-1	Filing date	24 July 1998 (24.07.1998)
VI-1-2	Number	Patent Application No. 10-208820
VI-1-3	Country	JP
VI-2	Priority claim of earlier national application	
VI-2-1	Filing date	07 August 1998 (07.08.1998)
VI-2-2	Number	Patent Application No. 10-224105
VI-2-3	Country	JP

PCT REQUEST

Original (for SUBMISSION) - printed on 16.07.1999 10:35:27 AM

VI-3	Priority claim of earlier national application		
VI-3-1	Filing date	25 August 1998 (25.08.1998)	
VI-3-2	Number	Patent Application No. 10-238116	
VI-3-3	Country	JP	
VI-4	Priority claim of earlier national application		
VI-4-1	Filing date	09 September 1998 (09.09.1998)	
VI-4-2	Number	Patent Application No. 10-254736	
VI-4-3	Country	JP	
VI-5	Priority claim of earlier national application		
VI-5-1	Filing date	29 September 1998 (29.09.1998)	
VI-5-2	Number	Patent Application No. 10-275505	
VI-5-3	Country	JP	
VII-1	International Searching Authority Chosen	European Patent Office (EPO) (ISA/EP)	
VIII	Check list	number of sheets	electronic file(s) attached
VIII-1	Request	5	-
VIII-2	Description (excluding sequence listing part)	121	-
VIII-3	Claims	1	-
VIII-4	Abstract	1	661102.txt
VIII-5	Drawings	50	-
VIII-6	Sequence listing part of description	177	-
VIII-7	TOTAL	355	
	Accompanying items	paper document(s) attached	electronic file(s) attached
VIII-8	Fee calculation sheet	✓	-
VIII-9	Separate signed power of attorney	✓	-
VIII-15	Nucleotide and/or amino acid sequence listing in computer readable form		separate diskette
VIII-16	PCT-EASY diskette	-	diskette
VIII-17	Other (specified):	Revenue stamps of transmittal fee for receiving office	-
VIII-17	Other (specified):	Certificate of payment of basic & designation fee for International Bureau	-
VIII-17	Other (specified):	Certificate of payment of search fee for EPO	-
VIII-18	Figure of the drawings which should accompany the abstract		
VIII-19	Language of filing of the international application	English	
IX-1	Signature of applicant or agent		
IX-1-1	Name (LAST, First)	AOYAMA, Tamiotsu	

PCT REQUEST

661102

Original (for SUBMISSION) - printed on 16.07.1999 10:35:27 AM

FOR RECEIVING OFFICE USE ONLY

10-1	Date of actual receipt of the purported international application	
10-2	Drawings:	
10-2-1	Received	
10-2-2	Not received	
10-3	Corrected date of actual receipt due to later but timely received papers or drawings completing the purported international application	
10-4	Date of timely receipt of the required corrections under PCT Article 11(2)	
10-5	International Searching Authority	ISA/EP
10-6	Transmittal of search copy delayed until search fee is paid	

FOR INTERNATIONAL BUREAU USE ONLY

11-1	Date of receipt of the record copy by the International Bureau	
------	--	--

PCT (ANNEX - FEE CALCULATION SHEET)

661102

Original (for SUBMISSION) - printed on 16.07.1999 10:35:27 AM

(This sheet is not part of and does not count as a sheet of the international application)

0	For receiving Office use only	
0-1	International Application No.	
0-2	Date stamp of the receiving Office	
0-4	Form - PCT/RO/101 (Annex)	
0-4-1	PCT Fee Calculation Sheet Prepared using	PCT-EASY Version 2.84 (updated 01.07.1999)
0-9	Applicant's or agent's file reference	661102
2	Applicant	SAGAMI CHEMICAL RESEARCH CENTER, et al.
12	Calculation of prescribed fees	fee amount/multiplier total amounts (JPY)
12-1	Transmittal fee T	⇒ 18,000
12-2	Search fee S	⇒ 120,000
12-3	International fee Basic fee (first 30 sheets) b1	54,800
12-4	Remaining sheets	325
12-5	Additional amount (X)	1,300
12-6	Total additional amount b2	422,500
12-7	b1 + b2 = B	477,300
12-8	Designation fees Number of designations contained in international application	78
12-9	Number of designation fees payable (maximum 10)	10
12-10	Amount of designation fee (X)	12,600
12-11	Total designation fees D	126,000
12-12	PCT-EASY fee reduction R	-16,900
12-13	Total International fee (B+D-R) I	⇒ 586,400
12-17	TOTAL FEES PAYABLE (T+S+I+P)	⇒ 724,400
12-19	Mode of payment	Transmittal fee: revenue stamps Search fee: bank draft International fee: bank draft Priority document fee: revenue stamps

VALIDATION LOG AND REMARKS

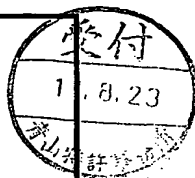
13-1-1	Applicant remarks Names	6214 Patent Attorney AOYAMA Tamotsu 6852 Patent Attorney TAMURA Yasuo 6703 Patent Attorney IWASAKI Mitsutaka
13-2-1	Validation messages Request	Green? The title of the invention should preferably be entered in capital letters. Please verify.

From the INTERNATIONAL SEARCHING AUTHORITY

PCT

To:

Aoyama & Partners
Attn. AOYAMA, T
IMP Building, 3-7, Shiromi
1-chome, Chuo-ku, Osaka-shi
Osaka 540-0001
JAPAN

NOTIFICATION OF RECEIPT
OF SEARCH COPY

(PCT Rule 25.1)

Date of mailing
(day/month/year)

20/08/1999

Applicant's or agent's file reference

661102

IMPORTANT NOTIFICATION

International application No.

PCT/JP 99/03929

International filing date(day/month/year)

22/07/1999

Priority date (day/month/year)

24/07/1998

Applicant

SAGAMI CHEMICAL RESEARCH CENTER et al.

1. Where the International Searching Authority and the Receiving Office are not the same office:

The applicant is hereby notified that the search copy of the international application was received by this International Searching Authority on the date indicated below.

Where the International Searching Authority and the Receiving Office are the same office:

The applicant is hereby notified that the search copy of the international application was received on the date indicated below.

05/08/1999 (date of receipt).

2. ☐ The search copy was accompanied by a nucleotide and/or amino acid sequence listing in computer readable form.

3. Time limit for establishment of International Search Report

The applicant is informed that the time limit for establishing the International Search Report is 3 months from the date of receipt indicated above or 9 months from the priority date, whichever time limit expires later

4. A copy of this notification has been sent to the International Bureau and, where the first sentence of paragraph 1 applies, to the Receiving Office.

Name and mailing address of the International Searching Authority



European Patent Office, P.B. 5818 Patentlaan 2
NL-2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl
Fax: (+31-70) 340-3016

Authorized officer

ISA/EP

TENT COOPERATION T A

PCT

NOTIFICATION OF ELECTION

(PCT Rule 61.2)

From the INTERNATIONAL BUREAU

To:

Assistant Commissioner for Patents
United States Patent and Trademark
Office
Box PCT
Washington, D.C.20231
ÉTATS-UNIS D'AMÉRIQUE

in its capacity as elected Office

Date of mailing (day/month/year) 01 March 2000 (01.03.00)	
International application No. PCT/JP99/03929	Applicant's or agent's file reference 661102
International filing date (day/month/year) 22 July 1999 (22.07.99)	Priority date (day/month/year) 24 July 1998 (24.07.98)
Applicant KATO, Seishi et al	

1. The designated Office is hereby notified of its election made:

☒ in the demand filed with the International Preliminary Examining Authority on:

03 February 2000 (03.02.00)

☐ in a notice effecting later election filed with the International Bureau on:
2. The election ☒ was
☐ was not

made before the expiration of 19 months from the priority date or, where Rule 32 applies, within the time limit under Rule 32.2(b).

The International Bureau of WIPO
34, chemin des Colombettes
1211 Geneva 20, Switzerland

Authorized officer

R. Forax

Facsimile No.: (41-22) 740.14.35

Telephone No.: (41-22) 338.83.38

From the INTERNATIONAL SEARCHING AUTHORITY

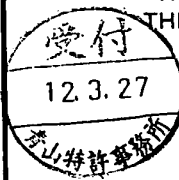
PCT

To:

Aoyama & Partners
Attn. AOYAMA, T
IMP Building, 3-7, Shiromi
1-chome, Chuo-ku, Osaka-shi
Osaka 540-0001
JAPAN

NOTIFICATION OF TRANSMITTAL OF
THE INTERNATIONAL SEARCH REPORT
OR THE DECLARATION

(PCT Rule 44.1)



Date of mailing
(day/month/year)

06/03/2000

Applicant's or agent's file reference

661102

FOR FURTHER ACTION

See paragraphs 1 and 4 below

International application No.

PCT/JP 99/ 03929

International filing date

(day/month/year)

22/07/1999

Applicant

SAGAMI CHEMICAL RESEARCH CENTER et al.

1. ☒ The applicant is hereby notified that the International Search Report has been established and is transmitted herewith.

Filing of amendments and statement under Article 19:

The applicant is entitled, if he so wishes, to amend the claims of the International Application (see Rule 46):

When? The time limit for filing such amendments is normally 2 months from the date of transmittal of the International Search Report; however, for more details, see the notes on the accompanying sheet.

Where? Directly to the International Bureau of WIPO
34, chemin des Colombettes
1211 Geneva 20, Switzerland
Facsimile No.: (41-22) 740.14.35

For more detailed instructions, see the notes on the accompanying sheet.

2. ☐ The applicant is hereby notified that no International Search Report will be established and that the declaration under Article 17(2)(a) to that effect is transmitted herewith.

3. ☐ With regard to the protest against payment of (an) additional fee(s) under Rule 40.2, the applicant is notified that:

☐ the protest together with the decision thereon has been transmitted to the International Bureau together with the applicant's request to forward the texts of both the protest and the decision thereon to the designated Offices.

☐ no decision has been made yet on the protest; the applicant will be notified as soon as a decision is made.

4. **Further action(s):** The applicant is reminded of the following:

Shortly after **18 months** from the priority date, the international application will be published by the International Bureau. If the applicant wishes to avoid or postpone publication, a notice of withdrawal of the international application, or of the priority claim, must reach the International Bureau as provided in Rules 90bis.1 and 90bis.3, respectively, before the completion of the technical preparations for international publication.

Within **19 months** from the priority date, a demand for international preliminary examination must be filed if the applicant wishes to postpone the entry into the national phase until 30 months from the priority date (in some Offices even later).

Within **20 months** from the priority date, the applicant must perform the prescribed acts for entry into the national phase before all designated Offices which have not been elected in the demand or in a later election within 19 months from the priority date or could not be elected because they are not bound by Chapter II.

Name and mailing address of the International Searching Authority



European Patent Office, P.B. 5818 Patentlaan 2
NL-2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Mireille Claudepierre

NOTES TO FORM PCT/ISA/220

These Notes are intended to give the basic instructions concerning the filing of amendments under article 19. The Notes are based on the requirements of the Patent Cooperation Treaty, the Regulations and the Administrative Instructions under that Treaty. In case of discrepancy between these Notes and those requirements, the latter are applicable. For more detailed information, see also the PCT Applicant's Guide, a publication of WIPO.

In these Notes, "Article", "Rule", and "Section" refer to the provisions of the PCT, the PCT Regulations and the PCT Administrative Instructions, respectively.

INSTRUCTIONS CONCERNING AMENDMENTS UNDER ARTICLE 19

The applicant has, after having received the international search report, one opportunity to amend the claims of the international application. It should however be emphasized that, since all parts of the international application (claims, description and drawings) may be amended during the international preliminary examination procedure, there is usually no need to file amendments of the claims under Article 19 except where, e.g. the applicant wants the latter to be published for the purposes of provisional protection or has another reason for amending the claims before international publication. Furthermore, it should be emphasized that provisional protection is available in some States only.

What parts of the international application may be amended?

Under Article 19, only the claims may be amended.

During the international phase, the claims may also be amended (or further amended) under Article 34 before the International Preliminary Examining Authority. The description and drawings may only be amended under Article 34 before the International Examining Authority.

Upon entry into the national phase, all parts of the international application may be amended under Article 28 or, where applicable, Article 41.

When?

Within 2 months from the date of transmittal of the international search report or 16 months from the priority date, whichever time limit expires later. It should be noted, however, that the amendments will be considered as having been received on time if they are received by the International Bureau after the expiration of the applicable time limit but before the completion of the technical preparations for international publication (Rule 46.1).

Where not to file the amendments?

The amendments may only be filed with the International Bureau and not with the receiving Office or the International Searching Authority (Rule 46.2).

Where a demand for international preliminary examination has been/is filed, see below.

How?

Either by cancelling one or more entire claims, by adding one or more new claims or by amending the text of one or more of the claims as filed.

A replacement sheet must be submitted for each sheet of the claims which, on account of an amendment or amendments, differs from the sheet originally filed.

All the claims appearing on a replacement sheet must be numbered in Arabic numerals. Where a claim is cancelled, no renumbering of the other claims is required. In all cases where claims are renumbered, they must be renumbered consecutively (Administrative Instructions, Section 205(b)).

The amendments must be made in the language in which the international application is to be published.

What documents must/may accompany the amendments?

Letter (Section 205(b)):

The amendments must be submitted with a letter.

The letter will not be published with the international application and the amended claims. It should not be confused with the "Statement under Article 19(1)" (see below, under "Statement under Article 19(1)").

The letter must be in English or French, at the choice of the applicant. However, if the language of the international application is English, the letter must be in English; if the language of the international application is French, the letter must be in French.

NOTES TO FORM PCT/ISA/220 (continued)

The letter must indicate the differences between the claims as filed and the claims as amended. It must, in particular, indicate, in connection with each claim appearing in the international application (it being understood that identical indications concerning several claims may be grouped), whether

- (i) the claim is unchanged;
- (ii) the claim is cancelled;
- (iii) the claim is new;
- (iv) the claim replaces one or more claims as filed;
- (v) the claim is the result of the division of a claim as filed.

The following examples illustrate the manner in which amendments must be explained in the accompanying letter:

1. [Where originally there were 48 claims and after amendment of some claims there are 51]:
"Claims 1 to 29, 31, 32, 34, 35, 37 to 48 replaced by amended claims bearing the same numbers; claims 30, 33 and 36 unchanged; new claims 49 to 51 added."
2. [Where originally there were 15 claims and after amendment of all claims there are 11]:
"Claims 1 to 15 replaced by amended claims 1 to 11."
3. [Where originally there were 14 claims and the amendments consist in cancelling some claims and in adding new claims]:
"Claims 1 to 6 and 14 unchanged; claims 7 to 13 cancelled; new claims 15, 16 and 17 added." or
"Claims 7 to 13 cancelled; new claims 15, 16 and 17 added; all other claims unchanged."
4. [Where various kinds of amendments are made]:
"Claims 1-10 unchanged; claims 11 to 13, 18 and 19 cancelled; claims 14, 15 and 16 replaced by amended claim 14; claim 17 subdivided into amended claims 15, 16 and 17; new claims 20 and 21 added."

"Statement under article 19(1)" (Rule 46.4)

The amendments may be accompanied by a statement explaining the amendments and indicating any impact that such amendments might have on the description and the drawings (which cannot be amended under Article 19(1)).

The statement will be published with the international application and the amended claims.

It must be in the language in which the international application is to be published.

It must be brief, not exceeding 500 words if in English or if translated into English.

It should not be confused with and does not replace the letter indicating the differences between the claims as filed and as amended. It must be filed on a separate sheet and must be identified as such by a heading, preferably by using the words "Statement under Article 19(1)."

It may not contain any disparaging comments on the international search report or the relevance of citations contained in that report. Reference to citations, relevant to a given claim, contained in the international search report may be made only in connection with an amendment of that claim.

Consequence if a demand for international preliminary examination has already been filed

If, at the time of filing any amendments and any accompanying statement, under Article 19, a demand for international preliminary examination has already been submitted, the applicant must preferably, at the time of filing the amendments (and any statement) with the International Bureau, also file with the International Preliminary Examining Authority a copy of such amendments (and of any statement) and, where required, a translation of such amendments for the procedure before that Authority (see Rules 55.3(a) and 62.2, first sentence). For further information, see the Notes to the demand form (PCT/IPEA/401).

Consequence with regard to translation of the international application for entry into the national phase

The applicant's attention is drawn to the fact that, upon entry into the national phase, a translation of the claims as amended under Article 19 may have to be furnished to the designated/elected Offices, instead of, or in addition to, the translation of the claims as filed.

For further details on the requirements of each designated/elected Office, see Volume II of the PCT Applicant's Guide.

PCT

INTERNATIONAL SEARCH REPORT

(PCT Article 18 and Rules 43 and 44)

Applicant's or agent's file reference 661102	FOR FURTHER ACTION see Notification of Transmittal of International Search Report (Form PCT/ISA/220) as well as, where applicable, item 5 below.	
International application No. PCT/JP 99/ 03929	International filing date (day/month/year) 22/07/1999	(Earliest) Priority Date (day/month/year) 24/07/1998
Applicant SAGAMI CHEMICAL RESEARCH CENTER et al.		

This International Search Report has been prepared by this International Searching Authority and is transmitted to the applicant according to Article 18. A copy is being transmitted to the International Bureau.

This International Search Report consists of a total of 10 sheets.
☐ It is also accompanied by a copy of each prior art document cited in this report.

1. Basis of the report

- a. With regard to the **language**, the international search was carried out on the basis of the international application in the language in which it was filed, unless otherwise indicated under this item.

☐ the international search was carried out on the basis of a translation of the international application furnished to this Authority (Rule 23.1(b)).

- b. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international search was carried out on the basis of the sequence listing :

☒ contained in the international application in written form.

☐ filed together with the international application in computer readable form.

☐ furnished subsequently to this Authority in written form.

☒ furnished subsequently to this Authority in computer readable form.

☒ the statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.

☒ the statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished

2. ☐ Certain claims were found unsearchable (See Box I).

3. ☒ Unity of invention is lacking (see Box II).

4. With regard to the **title**,

☒ the text is approved as submitted by the applicant.

☐ the text has been established by this Authority to read as follows:

5. With regard to the **abstract**,

☒ the text is approved as submitted by the applicant.

☐ the text has been established, according to Rule 38.2(b), by this Authority as it appears in Box III. The applicant may, within one month from the date of mailing of this international search report, submit comments to this Authority.

6. The figure of the **drawings** to be published with the abstract is Figure No.

☐ as suggested by the applicant.

☐ because the applicant failed to suggest a figure.

☐ because this figure better characterizes the invention.

☐ None of the figures.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: Claims 1-6 partially

A protein comprising amino acid sequence SEQ ID NO 1, a DNA SEQ ID NO 11 or 21, encoding this protein, as well as an expression vector capable of expressing this sequence and a eukaryotic cell expressing the DNA

2. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 2 and DNA SEQ ID 12 and 22

3. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 3 and DNA SEQ ID 13 and 23

4. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 4 and DNA SEQ ID 14 and 24

5. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 5 and DNA SEQ ID 15 and 25

6. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 6 and DNA SEQ ID 16 and 36

7. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 7 and DNA SEQ ID 17 and 37

8. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 8 and DNA SEQ ID 18 and 38

9. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 9 and DNA SEQ ID 19 and 39

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

10. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 10 and
DNA SEQ ID 20 and 30

11. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 31 and
DNA SEQ ID 41 and 51

12. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 32 and
DNA SEQ ID 42 and 52

13. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 33 and
DNA SEQ ID 43 and 53

14. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 34 and
DNA SEQ ID 44 and 54

15. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 35 and
DNA SEQ ID 45 and 55

16. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 36 and
DNA SEQ ID 46 and 56

17. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 37 and
DNA SEQ ID 47 and 57

18. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 38 and
DNA SEQ ID 48 and 58

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

19. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 39 and
DNA SEQ ID 49 and 59

20. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 40 and
DNA SEQ ID 50 and 60

21. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 61 and
DNA SEQ ID 71 and 81

22. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 62 and
DNA SEQ ID 72 and 82

23. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 63 and
DNA SEQ ID 73 and 83

24. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 64 and
DNA SEQ ID 74 and 84

25. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 65 and
DNA SEQ ID 75 and 85

26. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 66 and
DNA SEQ ID 76 and 86

27. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 67 and
DNA SEQ ID 77 and 87

28. Claims: 1-6 partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Idem as subject 1 but limited to protein SEQ ID NO. 68 and
DNA SEQ ID 78 and 88

29. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 69 and
DNA SEQ ID 79 and 89

30. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 70 and
DNA SEQ ID 80 and 90

31. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 91 and
DNA SEQ ID 101 and 111

32. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 92 and
DNA SEQ ID 102 and 112

33. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 93 and
DNA SEQ ID 103 and 113

34. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 94 and
DNA SEQ ID 104 and 114

35. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 95 and
DNA SEQ ID 105 and 115

36. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 96 and
DNA SEQ ID 106 and 116

37. Claims: 1-6 partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Idem as subject 1 but limited to protein SEQ ID NO. 97 and
DNA SEQ ID 107 and 117

38. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 98 and
DNA SEQ ID 108 and 118

39. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 99 and
DNA SEQ ID 109 and 119

40. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 100 and
DNA SEQ ID 110 and 120

41. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 121 and
DNA SEQ ID 131 and 141

42. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 122 and
DNA SEQ ID 132 and 142

43. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 123 and
DNA SEQ ID 133 and 143

44. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 124 and
DNA SEQ ID 134 and 144

45. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 125 and
DNA SEQ ID 135 and 145

46. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 126 and

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

DNA SEQ ID 136 and 146

47. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 127 and
DNA SEQ ID 137 and 147

48. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 128 and
DNA SEQ ID 138 and 148

49. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 129 and
DNA SEQ ID 139 and 149

50. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 130 and
DNA SEQ ID 140 and 150

INTERNATIONAL SEARCH REPORT

International Application No
PCT/JP 99/03929

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/12 C07K14/705 C12N5/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 21328 A (KATO SEISHI ;PROTEGENE INC (JP); SEKINE SHINGO (JP); SAGAMI CHEM R) 22 May 1998 (1998-05-22) abstract page 17, last paragraph -page 18, paragraph 1	1-6
X	--- DATABASE EMBLEMEST6 [Online] Accession Number AI057511, 22 July 1998 (1998-07-22) STRAUSBERG R: "H. sapiens cDNA clone IMAGE:1653181 3' similar to SW:YJK4 yeast P42929 hypothetical 16.2 kD protein in SME1-MEF2 intergenic region" XP002123564 100% identity in 357 BP overlap with SEQ ID NO:11 --- -/-	1-6

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

G document member of the same patent family

Date of the actual completion of the international search

23 November 1999

Date of mailing of the international search report

06.03.00

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

CUPIDO, M

INTERNATIONAL SEARCH REPORT

International Application No

PCT/JP 99/03929

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBLEST21 [Online] Accession Number AA 482452, 24 June 1997 (1997-06-24) HILLIER L ET AL.: "zv05b11.r1 Soares NhhMPu S1 Homo sapiens cDNA clone 7527733 5'similar to SW:YJK4 yeast P42929 hypothetical 16.2 kD protein in SME1-MEF2 intergenic region" XP002123565 99.7% identity in 367 BP overlap with SEQ ID NO 11</p>	1-6
A	<p>--- D'ANDREA ET AL: "Molecular Cloning of NKB1. A Natural Killer Cell Receptor for HLA -B Allotypes" JOURNAL OF IMMUNOLOGY, vol. 155, no. 5, 1 September 1995 (1995-09-01), pages 2306-2310 2310, XP002111500 ISSN: 0022-1767 abstract page 2307, right-hand column, line 16</p>	1-6
A	<p>--- GILLEN C M ET AL: "Molecular cloning and functional expression of the K-Cl cotransporter from rabbit, rat, and human." JOURNAL OF BIOLOGICAL CHEMISTRY., vol. 271, no. 27, 5 July 1996 (1996-07-05), pages 16237-16244, XP002119528 AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, BALTIMORE, MD., US ISSN: 0021-9258 abstract</p>	1-6
A	<p>--- KYTE J ET AL: "A SIMPLE METHOD FOR DISPLAYING THE HYDROPATHIC CHARACTER OF A PROTEIN" JOURNAL OF MOLECULAR BIOLOGY, vol. 157, no. 1, 5 May 1982 (1982-05-05), pages 105-132, XP000609692 ISSN: 0022-2836 cited in the application the whole document</p>	1-6
P,X	<p>--- DATABASE EMBLEST11 [Online] Accession Number AI 553893, 25 March 1999 (1999-03-25) STRAUSBERG R: "Homo sapiens cDNA clone IMAGE:2169115 3" XP002123566 100% identity in 375 BP overlap with SEQ ID 11</p> <p>-----</p>	1-6

Effect on patent family members

International Application No

PCI/JP 99/03929

Form PCT/ISA/210 (patent family annex) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP 99/ 03929

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheets

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-6 partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification⁷ : C12N 15/12, C07K 14/705, C12N 5/10	A3	(11) International Publication Number: WO 00/05367 (43) International Publication Date: 3 February 2000 (03.02.00)															
(21) International Application Number: PCT/JP99/03929 (22) International Filing Date: 22 July 1999 (22.07.99) (30) Priority Data: <table border="0"> <tr> <td>10/208820</td> <td>24 July 1998 (24.07.98)</td> <td>JP</td> </tr> <tr> <td>10/224105</td> <td>7 August 1998 (07.08.98)</td> <td>JP</td> </tr> <tr> <td>10/238116</td> <td>25 August 1998 (25.08.98)</td> <td>JP</td> </tr> <tr> <td>10/254736</td> <td>9 September 1998 (09.09.98)</td> <td>JP</td> </tr> <tr> <td>10/275505</td> <td>29 September 1998 (29.09.98)</td> <td>JP</td> </tr> </table> (71) Applicants (for all designated States except US): SAGAMI CHEMICAL RESEARCH CENTER [JP/JP]; 4-1, Nishi-Ohnuma 4-chome, Sagamihara-shi, Kanagawa 229-0012 (JP). PROTEGENE INC. [JP/JP]; 2-20-3, Naka-cho, Meguro-ku, Tokyo 153-0065 (JP). (72) Inventors; and (75) Inventors/Applicants (for US only): KATO, Seishi [JP/JP]; 3-46-50, Wakamatsu, Sagamihara-shi, Kanagawa 229-0014 (JP). KIMURA, Tomoko [JP/JP]; 302, 4-1-28, Nishiikuta, Tama-ku, Kawasaki-shi, Kanagawa 214-0037 (JP).		10/208820	24 July 1998 (24.07.98)	JP	10/224105	7 August 1998 (07.08.98)	JP	10/238116	25 August 1998 (25.08.98)	JP	10/254736	9 September 1998 (09.09.98)	JP	10/275505	29 September 1998 (29.09.98)	JP	(74) Agents: AOYAMA, Tamotsu et al.; Aoyama & Partners, IMP Building, 3-7, Shiromi 1-chome, Chuo-ku, Osaka-shi, Osaka 540-0001 (JP). (81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 4 May 2000 (04.05.00)
10/208820	24 July 1998 (24.07.98)	JP															
10/224105	7 August 1998 (07.08.98)	JP															
10/238116	25 August 1998 (25.08.98)	JP															
10/254736	9 September 1998 (09.09.98)	JP															
10/275505	29 September 1998 (29.09.98)	JP															
(54) Title: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE PROTEINS (57) Abstract <p>The present invention provides human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as well as eucaryotic cells expressing these DNAs.</p>																	

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(54) Title: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE PROTEINS			
(57) Abstract The present invention provides human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as well as eucaryotic cells expressing these DNAs.			

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DESCRIPTION

Human Proteins Having Hydrophobic
Domains and DNAs Encoding These Proteins

5

TECHNICAL FIELD

The present invention relates to human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as well as eucaryotic
10 cells expressing these DNAs. The proteins of the present invention can be employed as pharmaceuticals or as antigens for preparing antibodies against these proteins. The human cDNAs of the present invention can be utilized as probes for the genetic diagnosis and gene sources for the gene therapy.
15 Furthermore, the cDNAs can be utilized as gene sources for large-scale production of the proteins encoded by these cDNAs. Cells into which these genes are introduced to express secretory proteins and membrane proteins in large amounts can be utilized for detection of the corresponding
20 receptors and ligands, screening of novel low-molecular pharmaceuticals, and so on.

BACKGROUND ART

Cells secrete many proteins outside the cells. These
25 secretory proteins play important roles for the proliferation control, the differentiation induction, the material transportation, the biological protection, etc. in the cells. Different from intracellular proteins, the secretory proteins exert their actions outside the cells,
30 whereby they can be administered in the intracorporeal manner such as the injection or the drip, so that there are

hidden potentialities as medicines. In fact, a number of human secretory proteins such as interferons, interleukins, erythropoietin, thrombolytic agents, etc. have been currently employed as medicines. In addition, secretory proteins other than those described above have been undergoing clinical trials to develop as pharmaceuticals. Because it has been conceived that the human cells still produce many unknown secretory proteins, availability of these secretory proteins as well as genes coding for them is expected to lead to development of novel pharmaceuticals utilizing these proteins.

On the other hand, membrane proteins play important roles, as signal receptors, ion channels, transporters, etc. in the material transportation and the information transmission through the cell membrane. Examples thereof include receptors for a variety of cytokines, ion channels for the sodium ion, the potassium ion, the chloride ion, etc., transporters for saccharides and amino acids, and so on, where the genes for many of them have been cloned already. It has been clarified that abnormalities of these membrane proteins are associated with a number of hitherto-cryptogenic diseases. Therefore, discovery of a new membrane protein is anticipated to lead to elucidation of the causes of many diseases, so that isolation of a new gene coding for the membrane protein has been desired.

Heretofore, owing to difficulty in the purification from human cells, these secretory proteins and membrane proteins have been isolated by an approach from the gene side. A general method is the so-called expression cloning which comprises introduction of a cDNA library into eucaryotic cells to express cDNAs and then screening of the cells secreting, or expressing on the surface of membrane,

the objective active protein. However, this method is applicable only to cloning of a gene for a protein with a known function.

5 In general, secretory proteins and membrane proteins possess at least one hydrophobic domain inside the proteins, wherein, after synthesis thereof in the ribosome, this domain works as a secretory signal or remains in the phospholipid membrane to be trapped in the membrane. Accordingly, the evidence of this cDNA for encoding a
10 secretory protein and a membrane protein is provided by determination of the whole base sequence of a full-length cDNA followed by detection of highly hydrophobic domain(s) in the amino acid sequence of the protein encoded by this cDNA.

15

OBJECTS OF THE INVENTION

The main object of the present invention is to provide novel human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as
20 well as transformed eucaryotic cells that are capable of expressing these DNAs. This object as well as other objects and advantages of the present invention will become apparent to those skilled in the art from the following description with reference to the accompanying drawings.

25

BRIEF DESCRIPTION OF DRAWINGS

Fig. 1 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01550.

Fig. 2 illustrates the hydrophobicity/hydrophilicity
30 profile of the protein encoded by clone HP02593.

Fig. 3 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10195.

Fig. 4 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10423.

Fig. 5 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10506.

5 Fig. 6 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10507.

Fig. 7 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10548.

10 Fig. 8 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10566.

Fig. 9 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10567.

Fig. 10 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10568.

15 Fig. 11 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01426.

Fig. 12 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02515.

20 Fig. 13 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02575.

Fig. 14 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10357.

Fig. 15 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10447.

25 Fig. 16 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10477.

Fig. 17 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10513.

30 Fig. 18 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10540.

Fig. 19 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10557.

Fig. 20 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10563.

Fig. 21 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01467.

5 Fig. 22 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01956.

Fig. 23 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02545.

10 Fig. 24 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02551.

Fig. 25 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02631.

Fig. 26 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02632.

15 Fig. 27 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10488.

Fig. 28 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10538.

20 Fig. 29 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10542.

Fig. 30 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10571.

Fig. 31 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01470.

25 Fig. 32 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02419.

Fig. 33 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02631.

30 Fig. 34 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02695.

Fig. 35 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10031.

Fig. 36 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10530.

Fig. 37 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10541.

5 Fig. 38 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10550.

Fig. 39 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10590.

10 Fig. 40 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10591.

Fig. 41 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01462.

Fig. 42 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02485.

15 Fig. 43 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02798.

Fig. 44 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10041.

20 Fig. 45 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10246.

Fig. 46 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10392.

Fig. 47 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10489.

25 Fig. 48 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10519.

Fig. 49 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10531.

30 Fig. 50 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10574.

SUMMARY OF THE INVENTION

As the result of intensive studies, the present inventors have been successful in cloning of cDNAs coding for proteins having hydrophobic domains from the human full-length cDNA bank, thereby completing the present invention.

5 In other words, the present invention provides human proteins having hydrophobic domains, namely proteins comprising any of the amino acid sequences represented by SEQ ID Nos. 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130. Moreover, the present invention provides DNAs coding

10 for the above-mentioned proteins, exemplified by cDNAs comprising any of the base sequences represented by SEQ ID Nos. 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140, as well as expression vectors that are capable of expressing any of these DNAs by in vitro translation or in

15 eucaryotic cells and transformed eucaryotic cells that are capable of expressing these DNAs and of producing the above-mentioned proteins.

DETAILED DESCRIPTION OF THE INVENTION

20 The proteins of the present invention can be obtained, for example, by a method for isolation from human organs, cell lines, etc., a method for preparation of peptides by the chemical synthesis, or a method for production with the recombinant DNA technology using the DNAs coding for the

25 hydrophobic domains of the present invention, among which the method for production with the recombinant DNA technology is employed preferably. For instance, in vitro expression of the proteins can be achieved by preparation of an RNA by in vitro transcription from a vector having one of

30 the cDNAs of the present invention, followed by in vitro translation using this RNA as a template. Also, introduction of the translated region into a suitable expression vector

by the method known in the art leads to expression of a large amount of the encoded protein in prokaryotic cells such as *Escherichia coli*, *Bacillus subtilis*, etc., and eucaryotic cells such as yeasts, insect cells, mammalian cells, etc.

In the case where one of the proteins of the present invention is produced by expressing the DNA by in vitro translation, the protein of the present invention can be produced in vitro, when the translated region of this cDNA is introduced into a vector having an RNA polymerase promoter, followed by addition of the vector to an in vitro translation system such as a rabbit reticulocyte lysate or a wheat germ extract, containing an RNA polymerase corresponding to the promoter. RNA polymerase promoters are exemplified by T7, T3, SP6, and the like. The vectors containing these RNA polymerase promoters are exemplified by pKA1, pCDM8, pT3/T7 18, pT7/3 19, pBluescript II, and so on. Furthermore, the protein of the present invention can be expressed as the secreted form or the form incorporated into the microsome membrane, when a canine pancreas microsome or the like is added to the reaction system.

In the case where one of the protein of the present invention is produced by expressing the DNA in a microorganism such as *Escherichia coli* etc., a recombinant expression vector bearing the translated region of the cDNA of the present invention is constructed in an expression vector having an origin which can be replicated in the microorganism, a promoter, a ribosome-binding site, a cDNA-cloning site, a terminator etc. and, after transformation of the host cells with this expression vector, the resulting transformant is incubated, whereby the protein encoded by said cDNA can be produced on a large scale in the

microorganism. In this case, a protein fragment containing any region can be obtained by carrying out the expression with inserting an initiation codon and a termination codon in front of and behind the selected translated region.

5 Alternatively, a fusion protein with another protein can be expressed. Only the portion of the protein encoded by this cDNA can be obtained by cleavage of this fusion protein with a suitable protease. The expression vector for *Escherichia coli* is exemplified by the pUC series, pBluescript II, the

10 pET expression system, the pGEX expression system, and so on.

In the case where one of the proteins of the present invention is produced by expressing the DNA in eucaryotic cells, the protein of the present invention can be produced as a secretory protein or as a membrane protein on the cell-

15 membrane surface, when the translated region of this cDNA is introduced into an expression vector for eucaryotic cells that has a promoter, a splicing region, a poly(A) addition site, etc., followed by introduction into the eucaryotic cells. The expression vector is exemplified by pKA1,

20 pED6dpc2, pCDM8, pSVK3, pMSG, pSVL, pBK-CMV, pBK-RSV, EBV vector, pRS, pYES2, and so on. Examples of eucaryotic cells to be used in general include mammalian cultured cells such as simian kidney cells COS7, Chinese hamster ovary cells CHO, etc., budding yeasts, fission yeasts, silkworm cells,

25 *Xenopus* oocytes, and so on, but any eucaryotic cells may be used, provided that they are capable of expressing the proteins of the present invention. The expression vector can be introduced into the eucaryotic cells by methods known in the art such as the electroporation method, the calcium

30 phosphate method, the liposome method, the DEAE-dextran method, and so on.

After one of the proteins of the present invention is

expressed in prokaryotic cells or eucaryotic cells, the objective protein can be isolated from the culture and purified by a combination of separation procedures known in the art. Such examples include treatment with a denaturing agent such as urea or a detergent, sonication, enzymatic digestion, salting-out or solvent precipitation, dialysis, centrifugation, ultrafiltration, gel filtration, SDS-PAGE, isoelectric focusing, ion-exchange chromatography, hydrophobic chromatography, affinity chromatography, reverse phase chromatography, and so on.

The proteins of the present invention include peptide fragments (5 amino acid residues or more) containing any partial amino acid sequence in the amino acid sequences represented by SEQ ID Nos. 1. to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130. These peptide fragments can be utilized as antigens for preparation of antibodies. Hereupon, among the proteins of the present invention, those having the signal sequences are secreted in the form of mature proteins, after the signal sequences are removed. Therefore, these mature proteins shall come within the scope of the present invention. The N-terminal amino acid sequences of the mature proteins can be easily determined by using the method for the determination of cleavage site of a signal sequence [JP 8-187100 A]. Furthermore, some membrane proteins undergo the processing on the cell surface to be converted to the secretory forms. Such proteins or peptides in the secretory forms shall come within the scope of the present invention. In the case where sugar chain-binding sites are present in the amino acid sequences, expression in appropriate eucaryotic cells affords proteins to which sugar chains are attached. Accordingly, such proteins or peptides to which sugar chains are attached shall come within the

scope of the present invention.

The DNAs of the present invention include all the DNAs coding for the above-mentioned proteins. These DNAs can be obtained by using a method by chemical synthesis, a method
5 by cDNA cloning, and so on.

The cDNAs of the present invention can be cloned, for example, from cDNA libraries derived from the human cells. These cDNAs are synthesized by using as templates poly(A)⁺ RNAs extracted from human cells. The human cells may be
10 cells delivered from the human body, for example, by the operation or may be the cultured cells. The cDNAs can be synthesized by using any method selected from the Okayama-Berg method [Okayama, H. and Berg, P., Mol. Cell. Biol. 2: 161-170 (1982)], the Gubler-Hoffman method [Gubler, U. and
15 Hoffman, J. Gene 25: 263-269 (1983)], and so on, but it is preferred to use the capping method [Kato, S. et al., Gene 150: 243-250 (1994)], as exemplified in Examples, in order to obtain a full-length clone in an effective manner. In addition, commercially available, human cDNA libraries can
20 be utilized. Cloning of the cDNAs of the present invention from the cDNA libraries can be carried out by synthesis of an oligonucleotide on the basis of base sequences of any portion in the cDNA of the present invention, followed by screening using this oligonucleotide as the probe according
25 to the colony or plaque hybridization by a method known in the art. In addition, the cDNA fragments of the present invention can be prepared by synthesis of oligonucleotides which hybridize with both termini of the objective cDNA fragment, followed by the usage of these oligonucleotides as
30 the primers for the RT-PCR method using an mRNA isolated from human cells.

The cDNAs of the present invention are characterized by

comprising either of the base sequences represented by SEQ ID Nos. 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140 or the base sequences represented by SEQ ID Nos. 21 to 30, 51 to 60, 81 to 90, 111 to 120, and 141 to 150. Table 1
5 summarizes the clone number (HP number), the cells from which the cDNA was obtained, the total base number of the cDNA, and the number of the amino acid residues of the encoded protein, for each of the cDNAs.

Table 1

SEQ ID No.	HP number	Cells	Base number	Number of amino acid residues
1, 11, 21	HP01550	Stomach cancer	510	125
2, 12, 22	HP02593	Saos-2	697	131
3, 13, 23	HP10195	HT-1080	1619	242
4, 14, 24	HP10423	U-2 OS	1066	264
5, 15, 25	HP10506	Stomach cancer	618	112
6, 16, 26	HP10507	Stomach cancer	1021	146
7, 17, 27	HP10548	Stomach cancer	1432	344
8, 18, 28	HP10566	Stomach cancer	601	97
9, 19, 29	HP10567	Stomach cancer	585	124
10, 20, 30	HP10568	Stomach cancer	1100	327
31, 41, 51	HP01426	Stomach cancer	1065	313
32, 42, 52	HP02515	Saos-2	937	229
33, 43, 53	HP02575	Saos-2	1678	467
34, 44, 54	HP10357	Stomach cancer	467	99
35, 45, 55	HP10447	Liver	875	189
36, 46, 56	HP10477	Liver	1256	363
37, 47, 57	HP10513	Stomach cancer	884	249
38, 48, 58	HP10540	Saos-2	589	98
39, 49, 59	HP10557	Stomach cancer	673	172
40, 50, 60	HP10563	Saos-2	1425	120
61, 71, 81	HP01467	HT-1080	1436	307
62, 72, 82	HP01956	Liver	997	183
63, 73, 83	HP02545	Saos-2	1753	327
64, 74, 84	HP02551	Saos-2	1117	223
65, 75, 85	HP02631	Saos-2	1380	48
66, 76, 86	HP02632	HT-1080	1503	371
67, 77, 87	HP10488	Liver	733	90
68, 78, 88	HP10538	Saos-2	3768	499
69, 79, 89	HP10542	Stomach cancer	770	106
70, 80, 90	HP10571	Stomach cancer	1229	152

91, 101, 111	HP01470	Stomach cancer	1619	358
92, 102, 112	HP02419	Stomach cancer	2054	226
93, 103, 113	HP02631	Saos-2	1380	195
94, 104, 114	HP02695	Stomach cancer	1292	339
95, 105, 115	HP10031	Saos-2	2168	487
96, 106, 116	HP10530	Saos-2	1357	393
97, 107, 117	HP10541	Stomach cancer	711	196
98, 108, 118	HP10550	Stomach cancer	651	107
99, 109, 119	HP10590	HT-1080	1310	350
100, 110, 120	HP10591	HT-1080	1400	107
121, 131, 141	HP01462	HT-1080	2050	483
122, 132, 142	HP02485	Stomach cancer	2746	334
123, 133, 143	HP02798	HT-1080	1136	267
124, 134, 144	HP10041	Saos-2	619	106
125, 135, 145	HP10246	KB	864	224
126, 136, 146	HP10392	U-2 OS	1527	258
127, 137, 147	HP10489	Stomach cancer	659	110
128, 138, 148	HP10519	Stomach cancer	710	91
129, 139, 149	HP10531	Saos-2	2182	344
130, 140, 150	HP10574	Stomach cancer	2773	428

Hereupon, the same clones as the cDNAs of the present invention can be easily obtained by screening of the cDNA libraries constructed from the human cell lines or human tissues utilized in the present invention by the use of an oligonucleotide probe synthesized on the basis of the cDNA base sequence described in any of SEQ ID Nos. 11 to 30, 41 to 60, 71 to 90, 101 to 120, and 131 to 150.

In general, the polymorphism due to the individual difference is frequently observed in human genes. Accordingly, any cDNA in which one or plural nucleotides are inserted, deleted and/or substituted with other nucleotides in SEQ ID Nos. 11 to 30, 41 to 60, 71 to 90, 101 to 120, and

131 to 150 shall come within the scope of the present invention.

In a similar manner, any protein in which one or plural amino acids are inserted, deleted and/or substituted with other amino acids shall come within the scope of the present invention, as far as the protein possesses the activity of any protein having the amino acid sequences represented by SEQ ID Nos. 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130.

The cDNAs of the present invention include cDNA fragments (10 bp or more) containing any partial base sequence in the base sequences represented by SEQ ID Nos. 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140 or in the base sequences represented by SEQ ID Nos. 21 to 30, 51 to 60, 81 to 90, 111 to 120, and 141 to 150. Also, DNA fragments consisting of a sense strand and an anti-sense strand shall come within this scope. These DNA fragments can be utilized as the probes for the genetic diagnosis.

In addition to the activities and uses described above, the polynucleotides and proteins of the present invention may exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant

protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine

levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be

administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular

Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of
5 spleen cells, lymph node cells or thymocytes include,
without limitation, those described in: Polyclonal T cell
stimulation, Kruisbeek, A.M. and Shevach, E.M. In Current
Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp.
3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and
10 Measurement of mouse and human Interferon γ , Schreiber, R.D.
In Current Protocols in Immunology. J.E.e.a. Coligan eds.
Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of
hematopoietic and lymphopoietic cells include, without
15 limitation, those described in: Measurement of Human and
Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis,
L.S. and Lipsky, P.E. In Current Protocols in Immunology.
J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and
Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-
20 1211, 1991; Moreau et al., Nature 336:690-692, 1988;
Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-
2938, 1983; Measurement of mouse and human interleukin 6-
Nordan, R. In Current Protocols in Immunology. J.E.e.a.
Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons,
25 Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A.
83:1857-1861, 1986; Measurement of human Interleukin 11 -
Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J.
In Current Protocols in Immunology. J.E.e.a. Coligan eds.
Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991;
30 Measurement of mouse and human Interleukin 9 - Ciarletta, A.,
Giannotti, J., Clark, S.C. and Turner, K.J. In Current
Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp.

6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp.

and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

5 Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune
10 thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly
15 allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

 Using the proteins of the invention it may also be
20 possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by
25 suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing
30 non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent

has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen
5 functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD).
10 For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the
15 transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an
20 activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen
25 function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by
30 B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or

tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating

autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the commoncold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the

transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

5 In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can
10 be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the
15 expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell.
20 Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary
25 costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected
30 with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β microglobulin protein or an MHC class

II chain protein and an MHC class II chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J.

Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

5 Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J.J. and Brunswick, M. In
10 Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly
15 Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse
20 Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that
25 activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine
30 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965,

1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

5 Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808,
10 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology
15 1:639-648, 1992.

 Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et
20 al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

 A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the
25 treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells
30 alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to

stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and

Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is

not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

10 A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

20 Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and

in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head

trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

5 Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

10 It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including
15 vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

20 A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful
25 for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

30 Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon);

International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without
5 limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

10 A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of
15 follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals.
20 Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- group, may be useful as a fertility inducing therapeutic, based upon the
25 ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime
30 reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among

other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; 5 Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic 10 or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a 15 desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or 20 neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or 25 indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing 30 such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among

other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include,

without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22),

Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al.,
5 Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in
10 the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production
15 of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)),
20 ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over
25 production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for
30 immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A

protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues
5 necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth

10 Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria,
15 viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast
20 augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid,
25 protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and
30 violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of

embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Examples

The present invention is specifically illustrated in more detail by the following Examples, but Examples are not intended to restrict the present invention. The basic operations with regard to the recombinant DNA and the enzymatic reactions were carried out according to the literature ["Molecular Cloning. A Laboratory Manual", Cold Spring Harbor Laboratory, 1989]. Unless otherwise stated, restrictive enzymes and a variety of modification enzymes to be used were those available from Takara Shuzo. The buffer compositions and the reaction conditions for each of the enzyme reactions were as described in the manufacturer's instructions. The cDNA synthesis was carried out according to the literature [Kato, S. et al., Gene 150: 243-250 (1994)].

(1) Selection of cDNAs Encoding Proteins Having Hydrophobic Domains

The cDNA library of fibrosarcoma cell line HT-1080 (WO98/11217), the cDNA library of osteosarcoma cell line Saos-2 (WO97/33993), the cDNA library of osteosarcoma cell line U-2 OS (WO98/21328), the cDNA library of epidermoid

carcinoma cell line KB (WO98/11217), the cDNA library of tissues of stomach cancer delivered by the operation (WO98/21328), the cDNA library of liver tissue delivered by the operation (WO98/21328), and were used for the cDNA libraries. Full-length cDNA clones were selected from respective libraries and the whole base sequences thereof were determined to construct a homo-protein cDNA bank consisting of the full-length cDNA clones. The hydrophobicity/hydrophilicity profiles were determined for the proteins encoded by the full-length cDNA clones registered in the homo-protein cDNA bank by the Kyte-Doolittle method [Kyte, J. & Doolittle, R. F., J. Mol. Biol. 157: 105-132 (1982)] to examine the presence or absence of a hydrophobic region. Any clone that has a hydrophobic region being putative as a secretory signal or a transmembrane domain in the amino acid sequence of the encoded protein was selected as a clone candidate.

(2) Protein Synthesis by In Vitro Translation

The plasmid vector bearing the cDNA of the present invention was used for in vitro transcription/translation with a T_mT rabbit reticulocyte lysate kit (Promega). In this case, [³⁵S]methionine was added to label the expression product with a radioisotope. Each of the reactions was carried out according to the protocols attached to the kit. Two micrograms of the plasmid was subjected to the reaction at 30°C for 90 minutes in the reaction solution of a total volume of 25 µl containing 12.5 µl µ of T_mT rabbit reticulocyte lysate, 0.5 µl of a buffer solution (attached to the kit), 2 µl of an amino acid mixture (without methionine), 2 µl of [³⁵S]methionine (Amersham) (0.37 MBq/µl), 0.5 µl of T7 RNA polymerase, and 20 U of RNasin. Also, an experiment in the presence of a membrane system was carried

out by adding to this reaction system 2.5 μ l of a canine pancreas microsome fraction (Promega). To 3 μ l of the resulting reaction solution was added 2 μ l of the SDS sampling buffer (125 mM Tris-hydrochloric acid buffer, pH 6.8, 120 mM 2-mercaptoethanol, 2% SDS solution, 0.025% bromophenol blue, and 20% glycerol) and the resulting mixture was heated at 95°C for 3 minutes and then subjected to SDS-polyacrylamide gel electrophoresis. The molecular weight of the translation product was determined by carrying out the autoradiography.

(3) Expression by COS7

Escherichia coli cells bearing the expression vector for the protein of the present invention was incubated at 37°C for 2 hours in 2 ml of the 2xYT culture medium containing 100 μ g/ml of ampicillin, the helper phage M13K07 (50 μ l) was added, and the incubation was continued at 37°C overnight. A supernatant separated by centrifugation underwent precipitation with polyethylene glycol to obtain single-stranded phage particles. These particles were suspended in 100 μ l of 1 mM Tris-0.1 mM EDTA, pH 8 (TE).

The cultured cells derived from simian kidney, COS7, were incubated at 37°C in the presence of 5% CO₂ in the Dulbecco's modified Eagle's culture medium (DMEM) containing 10% fetal calf serum. Into a 6-well plate (Nunc, well diameter: 3 cm) were inoculated with 1×10^5 COS7 cells and incubation was carried out at 37°C for 22 hours in the presence of 5% CO₂. After the culture medium was removed, the cell surface was washed with a phosphate buffer solution and then washed again with DMEM containing 50 mM Tris-hydrochloric acid (pH 7.5) (TDMEM). To the resulting cells was added a suspension of 1 μ l of the single-stranded phage suspension, 0.6 ml of the DMEM culture medium, and 3 μ l of

TRANSFECTAM™ (IBF) and the resulting mixture was incubated at 37°C for 3 hours in the presence of 5% CO₂. After the sample solution was removed, the cell surface was washed with TDMEM, 2 ml per well of DMEM containing 10% fetal calf serum was added, and the incubation was carried out at 37°C for 2 days in the presence of 5% CO₂. After the culture medium was replaced by a culture medium containing [³⁵S]cystine or [³⁵S]methionine, the incubation was carried out for one hour. After the culture medium and the cells were separated by centrifugation, proteins in the culture medium fraction and the cell-membrane fraction were subjected to SDS-PAGE.

(4) Clone Examples

<HP01550> (SEQ ID Nos. 1, 11, and 21)

Determination of the whole base sequence of the cDNA insert of clone HP01550 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 65-bp 5'-untranslated region, a 378-bp ORF, and a 67-bp 3'-untranslated region. The ORF codes for a protein consisting of 125 amino acid residues and there existed one putative transmembrane domain. Figure 1 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 15 kDa that was almost identical with the molecular weight of 13,825 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein F45G2.c (GenBank Accession No. Z93382). Table 2 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the C.

5

Table 2

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25

<HP02593> (SEQ ID Nos. 2, 12, and 22)

30

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to a human OB-R gene-related protein (EMBL Accession No. Y12670). Table 3 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human OB-R gene-related protein (OB). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 67.9% in the entire region.

```

25 HP MAGIKALISLSFGGAIGLMLGLCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTD
    ***.***.***.***** ***** *.*****.*.*****.***.***.***.***
    OB MAGVKALVALSFSGAIGLTFMLGLCALEDYGVYWPLFVLIFHAISPIPHFIAKRVTYDSD
    HP AMSNACKELAIFLT TGIVVSAFGLPIVFARAH LIEWGACALVLTGNTVIFATILGFFLIVF
    * *.***.*** *.*****.***.***.***.***.***.***.***.***.***.***
    OB ATSSACRELAYFFT TGIVVSAFGFPVILARVAVIKWGACGLVLAGNAVIFLTIQGFFLIF
    HP GSNDDFSWQQW
    *.***.***
30 OB GRGDDFSWEOW

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Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA306490) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10195> (SEQ ID Nos. 3, 13, and 23)

Determination of the whole base sequence of the cDNA insert of clone HP10195 obtained from cDNA library of human fibrosarcoma HT-1080 revealed the structure consisting of a 286-bp 5'-untranslated region, a 729-bp ORF, and a 604-bp 3'-untranslated region. The ORF codes for a protein consisting of 242 amino acid residues and there existed one putative transmembrane domain at the C-terminus. Figure 3 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 32 kDa that was somewhat larger than the molecular weight of 27,300 predicted from the ORF. When expressed in COS7 cells, an expression product of about 21 kDa was observed in the supernatant fraction and the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein has revealed the registration of sequences that were similar to the Aplysia VAP-33 (SWISS-PROT Accession No. P53173). Table 4 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the Aplysia VAP-33 (AP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the

present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 46.5% in the entire region.

5

Table 4

	HP	MAKHEQILVLDPPTDLKFKGPFTDVVTNLKLRNPSDRKVCVKVKTAPRRYCVRPNSGI
		.* *.**.*...*.*****.***.***.*****.*****
10	AP	MASHEQALILEPAGELRFKGPFTDVVTADLKLSNPTDRRICFKVKVKTAPKRYCVRPNSGI
	HP	IDPGSTVTVSVMLQPFYDPNEKSKHKFMVQTIAPPNTSD-MEAVWKEAKPDELMDSKL
		..******.*****.*****..** .. . * .***. * ..***.***
	AP	LEPKTSIAVAVMLQPFNYDPNEKNKHKFMVQSMYAPDHVVESQELLWKDAPPESLMDTKL
	HP	RCVFEMPENNDKLNDMEPSK-----AVPLNASKQDGPMPKP-HSVSLNDTE
15		*****..... . ..*.* ... **. *.
	AP	RCVFEMPDGSHQAPASDASRATDAGAHFSESALEDPTVASRKTETQSPKRVGAVGSAGED
	HP	TRKLMEECKRLQGEMMKLSEENRHLRDEGLRLRKVAHSD--KPGSTSTASFRDNVTSLP
		..** . * *. *. * . * . * . * . * . * . * . * . * . * . * . * . * . *
	AP	VKKLQHELKKAQSEITSLKGENSEQLKDEGIRLRKVAMTDTVSPTPLNPSPAPAAVRAFP
20	HP	SLLVVIAAIFIGFFLGKFIL
		... * . * . * . * . * . * . * . *
	AP	PVVYVVAAILGLIIGKFL

25 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA447905) in ESTs, but, since they are partial sequences, it can not be judged whether or not

30 any of these sequences codes for the same protein as the protein of the present invention.

<HP10423> (SEQ ID Nos. 4, 14, and 24)

Determination of the whole base sequence of the cDNA insert of clone HP10423 obtained from cDNA library of human osteosarcoma cell line U-2 OS revealed the structure consisting of a 64-bp 5'-untranslated region, a 795-bp ORF, and a 207-bp 3'-untranslated region. The ORF codes for a protein consisting of 264 amino acid residues and there existed a secretory signal at the N-terminus and one putative transmembrane domain at the N-terminus. Figure 4 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was almost identical with the molecular weight of 29,377 predicted from the ORF. When expressed in COS7 cells, an expression product of about 31 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. D80116) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10506> (SEQ ID Nos. 5, 15, and 25)

Determination of the whole base sequence of the cDNA insert of clone HP10506 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 53-bp 5'-untranslated region, a 339-bp ORF, and a 226-bp 3'-untranslated region. The ORF codes for a protein consisting of 112 amino acid residues and there existed one putative transmembrane domain. Figure 5 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 11,821 predicted from the ORF. When expressed in
5 COS7 cells, an expression product of about 13 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for
10 example, Accession No. AA282544) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

15 <HP10507> (SEQ ID Nos. 6, 16, and 26)

Determination of the whole base sequence of the cDNA insert of clone HP10507 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 412-bp 5'-untranslated region, a 441-bp ORF, and a 168-bp 3'-
20 untranslated region. The ORF codes for a protein consisting of 146 amino acid residues and there existed a secretory signal at the N-terminus and one putative transmembrane domain at the C-terminus. Figure 6 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-
25 Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 19 kDa that was somewhat larger than the molecular weight of 16,347 predicted from the ORF.

Furthermore, the search of the GenBank using the base
30 sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA424759) in ESTs, but, since they

are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

5 <HP10548> (SEQ ID Nos. 7, 17, and 27)

Determination of the whole base sequence of the cDNA insert of clone HP10548 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 330-bp 5'-untranslated region, a 1035-bp ORF, and a 67-bp 3'-
10 untranslated region. The ORF codes for a protein consisting of 344 amino acid residues and there existed four putative transmembrane domains. Figure 7 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro
15 translation resulted in formation of a translation product of a high molecular weight.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for
20 example, Accession No. AA143152) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

25 <HP10566> (SEQ ID Nos. 8, 18, and 28)

Determination of the whole base sequence of the cDNA insert of clone HP10566 obtained from cDNA library of the human stomach cancer revealed the structure consisting of a 61-bp 5'-untranslated region, a 294-bp ORF, and a 246-bp 3'-
30 untranslated region. The ORF codes for a protein consisting of 97 amino acid residues and there existed one putative transmembrane domain at the C-terminus. Figure 8 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 11,452 predicted from the ORF. When expressed in COS7 cells, an expression product of about 12 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W79821) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10567> (SEQ ID Nos. 9, 19, and 29)

Determination of the whole base sequence of the cDNA insert of clone HP10567 obtained from cDNA library of the human stomach cancer revealed the structure consisting of a 77-bp 5'-untranslated region, a 375-bp ORF, and a 133-bp 3'-untranslated region. The ORF codes for a protein consisting of 124 amino acid residues and there existed one putative transmembrane domain at the C-terminus. Figure 9 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 14 kDa that was almost identical with the molecular weight of 14,484 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA428475) in ESTs, but, since they

are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

5 <HP10568> (SEQ ID Nos. 10, 20, and 30)

Determination of the whole base sequence of the cDNA insert of clone HP10568 obtained from cDNA library of the human stomach cancer revealed the structure consisting of a 56-bp 5'-untranslated region, a 984-bp ORF, and a 60-bp 3'-untranslated region. The ORF codes for a protein consisting of 327 amino acid residues and there existed a secretory signal at the N-terminus and one putative transmembrane domain at the C-terminus. Figure 10 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 36.5 kDa that was almost identical with the molecular weight of 34,326 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 40 kDa which is considered to have a sugar chain being attached. In addition, there exist in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Leu-Thr at position 138 and Asn-Leu-Ser at position 206). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from valine at position 24. When expressed in COS7 cells, an expression product of about 31 kDa was observed in the supernatant fraction and the membrane fraction.

30 The search of the protein data base using the amino acid sequence of the present protein has revealed that the protein was similar to the human cell-surface A33 antigen

(SWISS-PROT Accession No. Q99795). Table 5 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human cell-surface A33 antigen (A3). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 30.0% in the N-terminal region of 243 residues.

Table 5

	HP	MAELPGPFLCGALLGFLCLSGLADEVKVPTEPLSTPLGKTAELTCTYSTSVGDSFAL-EW	
			*. * * * *
15	A3	MVGKMWPVLWTLCAVRVTVD AISVETPQDVLRASQGKSVTLPC TYHTSTSSREGLIQW	
	HP	SFVQPGKPISESHPILYFTNGHLYPTGSKSKRVSL LQNPPTVGVATLKLTDVHPSDTGTY	
	 *	* *
	A3	DKLL--LTHTERVVIWPF SNKN-YIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTY	
	HP	LCQVNNPPDFYTNGLGLINLTVLVPPSNPLCSQSGQTSVGGSTALRCSSSEGAPKPVYNW	
20		* *	* *
	A3	ECSVSLMSDLEGNTKSRVRL LVLPSPKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSW	
	HP	VRLGTFPTSPGSMVQDEVSGQLILTNLSLTSSGTYRCVATNQMG SASCELTLSVTEPS-	
		* *	* *
	A3	KRYNILNQEQP--LAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSM	
25	HP	-QGRVAGALIGVLLGVLLLSVAAFCLVRFQKERGKKPKETYGGSDLREDAIAPGISEHTC	
	 *	
	A3	NVALYVGIAVGVAALIIIGIIIIYCCCCRGKDDNTEDKEDARPNREAYEEPPEQLRELSR	
	HP	MRADSSKGFLERPSSASTVTTTTSKSLPMVV	
30	A3	EREEEDDYRQEEQRSTGRES PDHLDQ	

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration

of sequences that shared a homology of 90% or more (for example, Accession No. T24595) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein
5 of the present invention.

<HP01426> (SEQ ID Nos. 31, 41, and 51)

Determination of the whole base sequence of the cDNA insert of clone HP01426 obtained from cDNA library of human
10 stomach cancer revealed the structure consisting of a 1-bp 5'-untranslated region, a 942-bp ORF, and a 122-bp 3'-untranslated region. The ORF codes for a protein consisting of 313 amino acid residues and there existed a putative secretory signal. Figure 11 depicts the
15 hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 36 kDa that was almost identical with the molecular weight of 34,955 predicted from the ORF. In this case, the
20 addition of a microsome led to the formation of a product of 38 kDa which is considered to have a sugar chain being attached after secretion. In addition, there exists in the amino acid sequence of this protein one site at which N-glycosylation may occur (Asn-Ser-Ser at position 163).
25 Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from tryptophan at position 17. When expressed in COS7 cells, an expression product of about 39 kDa was observed in the supernatant
30 fraction and the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the

protein was similar to the *Xenopus laevis* cortical granule lectin (EMBL Accession No. X82626). Table 6 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *X. laevis* cortical granule lectin (XL). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 67.9% in the region other than the N-terminal region.

Table 6

```

15  HP MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT
    *      **                      *      *****. . * **.* * .
XL  MLVHILLLLLVTTGGLSQSCEPVVIVASKNMVKQLDCDKFRSCKEIKDSNEEAQDGIYTLTS
HP  ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY
    .*. *****. .*****.* *****.*****.*****
20  XL SDGISYQTFCDMTTNGGGWTLVASVHENNMAGKCTIGDRWSSQQGNRADYPEGDGNWANY
HP  NTFGSAEAATSDDYKNPGYYDIAQKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG
    *****.*****.* .**.******.*. ***** ***.**.* *
XL  NTFGSAGGATSDDYKNPGYYDIEAYNLGVWHVPNKTPLSVWRNSSLQRYRTTDGILFKHG
HP  HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRV
    ***.**. ***** *.* .*.***.***.***.***.***.***
25  XL GNLFSLYRIYPVKYGIGSCSKDSGPTVPVVYDLGSAKLTASFYSPDFRSQFTPGYIQFRP
HP  FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSSS
    .*.*** ***.***.***.*** *****.*.*****.***.***
XL  INTEKAALALCPGMKMESC NVEHVCIGGGGYFPEADPRQCGDFAAYDFNGYGTKKFNSAG
HP  REITEAAVLLFYR
30  *****
XL  IEITEAAVLLFYL

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Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R06009) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02515> (SEQ ID Nos. 32, 42, and 52)

Determination of the whole base sequence of the cDNA insert of clone HP02515 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 176-bp 5'-untranslated region, a 690-bp ORF, and a 71-bp 3'-untranslated region. The ORF codes for a protein consisting of 229 amino acid residues and there existed a putative secretory signal at N-terminus and one putative transmembrane domain at the C-terminus. Figure 12 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was almost identical with the molecular weight of 26,000 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 25.5 kDa from which the secretory signal is considered to have been cleaved. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from phenylalanine at position 28.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human T1/ST2 receptor binding protein (GenBank Accession No. U41804). Table 7 shows the

comparison between amino acid sequences of the human protein of the present invention (HP) and the human T1/ST2 receptor binding protein (T1). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 55.8% in the entire region.

Table 7

```

HP  MGDKIWLFPFVLLLAALPPVLLPGAAGFTPSLSDSFTFTLPAGQKECFYQPMPLKASLE
      *.... ** .*** . *** . * ..*** ***.*****. * .****
T1  MMAAGAALALALWLL--MPPVEV-GGAGPPPIQDGEFTFLLPAGRKQCFYQSAPANASLE
15 HP  IEYQVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVE-TEVGDMFCFDNTFSTISEK
      .*****.*****.** *.***. * * * *.***** **.*...*****.*****
T1  TEYQVIGGAGLDVDFTLESPQGVLLVSESERKADGVHTVEPTTEAGDYKLCFDNSFSTISEK
HP  VIFFELILDNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLR
      ..*****.*... ..* * * . . .*****.* **.*...*****.***
20 T1  LVFFELIFDSL-QDDEVEGWAEAVEPEEMLDVKMEDIKESIETMRTRLERSIQMLTLRL
HP  AFEARDRNIQESNFDNRVNFWSMVNLVVMVVSAIQVYMLKSLFEDKRKSRT
      *****.*.*..***** **.*...*****. ....* **.*
T1  AFEARDRNLQEGNLERNVNFWSAVNVAVLLLVAVLQVCTLKRFFQDKRPVPT

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Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA381943) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02575> (SEQ ID Nos. 33, 43, and 53)

Determination of the whole base sequence of the cDNA insert of clone HP02575 obtained from cDNA library of human osteosarcome cell line Saos-2 revealed the structure consisting of a 55-bp 5'-untranslated region, a 1404-bp ORF, and a 219-bp 3'-untranslated region. The ORF codes for a protein consisting of 467 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 13 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 52 kDa that was almost identical with the molecular weight of 54,065 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 57 kDa which is considered to have a sugar chain being attached afetr secretion. In addition, there exist in the amino acid sequence of this protein three sites at which N-glycosylation may occur (Asn-Arg-Thr at position 171, Asn-Ser-Thr at position 239 and Asn-Asp-Thr at position 377). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from histidine at position 29. When expressed in COS7 cells, an expression product of about 55 kDa was observed in the supernatant fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human α -L-fucosidase (SWISS-PROT Accession No. P04066). Table 8 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human α -L-fucosidase (FC). Therein,

the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both
 5 proteins shared a homology of 54.8% in the entire region.

Table 8

	HP	MRPQELPRLAFPLLLLLLLLLLPPPPC-PAHSATRFDPTWESLDARQLPAWFDQAKFGIFI
10		.*****.* .. . *... *...* ***.*.....*****.*
	FC	MRSRPAGPALLLLLLLFLGAAESVRRRAQPPRRYTPDWPSLDSRPLPAWFDEAKFGVFI
	HP	HWGVFSVPSFGSEFWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWAD
		*****.*.....** * *.* ***.*****.*.....** *.....*
	FC	HWGVFSVPAWGSEFWWHWQGEGRPQYQRFMRDNYPFGFSYADFGPQFTARFFHPEEWAD
15	HP	IFQASGAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFLG
		.*.....** * * *****. * ***.* *.....* *.....*
	FC	LFQAAGAKYVVLTTKHHEGFTNWSPVSWNWSKDVGPHRDLVGELGTALRR-NIRYGL
	HP	YYSLFEFWHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWN
		*...*****.* *.....*.....* ...*****.*.....*****. . ** ***
20	FC	YHSLLEWFHPLYLLDKNGFKTQHVFSAKTMPELYDLVNSYKPDLIWSDGEWECPDITYWN
	HP	STGFLAWLYNESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDK
		...***.*.....*****... *.....*.....* * ***** * .***
	FC	STNFLSWLYNDSPVKDEVVVNDRWGQNCSCHHGGYNCEDKFKPQSLPDHKWEMCTSIDK
	HP	LSWGYRREAGISDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQMGSW
25		*****.* ..*****.*** *.....** * * ..***** ..*
	FC	FSWGYRRDMALSDVTEESEIISELVQTVSLGGNYLLNIGPTKDGLIVPIFQERLLAVGKW
	HP	LKVNGEAIYETHTWRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGA
	** * ..*.....*.....* *****.*.....* * * ..*
	FC	LSINGEAIYASKPWRVQWEKNTTSVWYTSKGSA--VYAIFLHWPENGVLNLESPITT-ST
30	HP	TEVKLLGHGQPLNWISLEQNGIMVELPQLTIHQMPCKKWGWALALTNI
	* ..*****. ..* ..*.....***
	FC	TKITMLGIQGDLKWSTDPDKGLFISLPQLPPSAVPAEFAWTIKLTGVK

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N28668) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

10 <HP10357> (SEQ ID Nos. 34, 44, and 54)

Determination of the whole base sequence of the cDNA insert of clone HP10357 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 113-bp 5'-untranslated region, a 300-bp ORF, and a 54-bp 3'-untranslated region. The ORF codes for a protein consisting of 99 amino acid residues and there existed two putative transmembrane domains. Figure 14 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 11 kDa that was almost identical with the molecular weight of 10,923 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA477156) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

30 <HP10447> (SEQ ID Nos. 35, 45, and 55)

Determination of the whole base sequence of the cDNA

insert of clone HP10447 obtained from cDNA library of human liver revealed the structure consisting of a 271-bp 5'-untranslated region, a 570-bp ORF, and a 34-bp 3'-untranslated region. The ORF codes for a protein consisting of 189 amino acid residues and there existed five putative transmembrane domains. Figure 15 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA296976) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10477> (SEQ ID Nos. 36, 46, and 56)

Determination of the whole base sequence of the cDNA insert of clone HP10477 obtained from cDNA library of human liver revealed the structure consisting of a 149-bp 5'-untranslated region, a 1092-bp ORF, and a 15-bp 3'-untranslated region. The ORF codes for a protein consisting of 363 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 16 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 40 kDa that was almost identical with the molecular weight of 39,884 predicted from the ORF.

The search of the protein data base using the amino

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Table 9

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30

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration

of sequences that shared a homology of 90% or more (for example, Accession No. AA424759) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10513> (SEQ ID Nos. 37, 47, and 57)

Determination of the whole base sequence of the cDNA insert of clone HP10513 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 134-bp 5'-untranslated region, a 750-bp ORF, and a 0-bp 3'-untranslated region. The ORF codes for a protein consisting of 249 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 17 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 29 kDa that was almost identical with the molecular weight of 27,373 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human hypothetical protein KIAA0512 (GenBank Accession No. AB011084). Table 10 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human hypothetical protein KIAA0512 (KI). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 31.6% in the C-terminal region of 196 amino acid residues.

consisting of a 47-bp 5'-untranslated region, a 297-bp ORF, and a 245-bp 3'-untranslated region. The ORF codes for a protein consisting of 98 amino acid residues and there existed two putative transmembrane domains. Figure 18 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein CEF49C12.12 (GenBank Accession No. Z68227). Table 11 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein CEF49C12.12 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 36.1% in the entire region.

Table 11

25	HP M-ASLLCCGPKLAACGIVLSAWGVIMLIMLGIFFNVHSAVLIEDVPFTEKDFENGPNQNIY
	* *** * * * * * * * * * * * *
	CE MGKICPLMGPKMSAFCMVMSVWGVIFLGLLGVFFYIQAVTLFPDLHF-EGHGKVPSSVID
	HP NLYEQVSYNCFIAAGLYLLLGGFSFCQVRLNKRKEYMVR
	* * * * * * * * * *
30	CE AKYNEKATQCWIAAGLYAVTLIAVFWQ---NKYNTAQIF

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA420715) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

10 <HP10557> (SEQ ID Nos. 39, 49, and 59)

Determination of the whole base sequence of the cDNA insert of clone HP10557 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 24-bp 5'-untranslated region, a 519-bp ORF, and a 130-bp 3'-untranslated region. The ORF codes for a protein consisting of 172 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 19 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 32 kDa that was larger than the molecular weight of 18,844 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 39 kDa which is considered to have been subjected to some modification after secretion. In addition, there exist in the amino acid sequence of this protein no site at which N-glycosylation may occur. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glycine at position 32. When expressed in COS7 cells, an expression product of about 20 kDa was observed in the supernatant fraction and the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human progesterone binding protein (EMBL Accession No. AJ002030). Table 12 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human progesterone binding protein (PG). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 30.5% in the C-terminal region of 151 amino acid residues.

Table 12

15	HP	MVG PAP
	PG MAAGDGDVKLGTLGSGSESSNDGGSESPGDAGAAAEAGGGWAAAALALLTGGGEMLLNVAL	
	HP RRRRLRPLAALALVLALAPGLPTARAGQTPRPAERGPPV--RLFTEEELARYGGEEEDQPI	
20	** * . . . * . * . * *	
	PG VALVLLGAYRLWVRWGRRGLGAGAGAGEESPATSLPRMKKRDFSLEQLRQYDG-SRNPRI	
	HP YLAVKGVVFDVTSKGFEFYGRGAPYNALTGKDSTRGVAKMSLDPADLTHDTTGLTAKELEA	
	. * **. * * * * *	
	PG LLAVNGKVFDVTKGSKFYGPAGPYGIFAGR DASRGLATFCLDKDALRDEYDDLSDLNAVQ	
25	HP LDEV--FTKVYKAKYPIVGYTARRILNEDGSPNLDKPEDQPHFDIKDEF	
	... * . . . * . * . * . * . . . * . . . * . . . * . . . *	
	PG MESVREWEMQFKEKY---DYVG-RLLKPGEEPS-EYTDEEDTKDHNKQD	

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for

example, Accession No. AA101709) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

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<HP10563> (SEQ ID Nos. 40, 50, and 60)

Determination of the whole base sequence of the cDNA insert of clone HP10563 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure
10 consisting of a 126-bp 5'-untranslated region, a 363-bp ORF, and a 936-bp 3'-untranslated region. The ORF codes for a protein consisting of 120 amino acid residues and there existed two putative transmembrane domains. Figure 20 depicts the hydrophobicity/hydrophilicity profile, obtained
15 by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 18.5 kDa that was larger than the molecular weight of 13,180 predicted from the ORF.

The search of the protein data base using the amino
20 acid sequence of the present protein revealed that the protein was similar to the Arabidopsis thaliana hypothetical protein F27F23.15 (GenBank Accession No. AC003058). Table 13 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the A.
25 thaliana hypothetical protein F27F23.15 (AT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins
30 shared a homology of 35.5% in the entire region.

Table 13

HP MMPSRTNLATGIPSSKVYSRLSSTDGYYIDLQFKKTPPKIPYKAIALATVLFLLIGAFLLI
 .. * * *.****. *.....*
 AT MAYVDHAFSISDEDLMIGTSY-TVSNRPPVKEISLAVGLLVFGTLGI
 HP IIGSLLLSGYISKGGADRAVPVLIIGILVFLPGFYHLRIAYYASKGYRGYSYDDIPDFDD
 ..* *. * *.****. ***** ***.*.****
 AT VLGFEMAYNRVG-GDRGHGIEFFIVLGLLFLPGFYTRIAYYAYKGYKGESFSNIPSV

10

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA083574) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP01467> (SEO ID Nos. 61, 71, and 81)

20

Determination of the whole base sequence of the cDNA insert of clone HP01467 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 65-bp 5'-untranslated region, a 924-bp ORF, and a 447-bp 3'-untranslated region. The ORF codes for a protein consisting of 307 amino acid residues and there existed three putative transmembrane domains. Figure 21 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

30

The search of the protein data base using the amino

acid sequence of the present protein revealed that the protein was similar to the rat Sec22 homologue (GenBank Accession No. U42209). Table 14 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the rat Sec22 homologue (RN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 94.6% in the N-terminal region of 241 amino acid residues. The protein of the present invention was longer by 53 amino acids at the C-terminus than the rat Sec22 homologue.

15

Table 14

	HP	MSMILSASVIRVRDGLPLSASTDYEQSTGMQECRKYFKMLSRKLAQLPDRCTLKTGHYNI
		*****.*****.***.*****.*****..**
	RN	MSMILSASVVRVRDGLPLSASTDCEQSAGVQECRKYFKMLSRKLAQFPDRCTLKTGRHNI
20	HP	NFISSLGVS YMMMLCTENYPNVLA FSFLDELQKEFITTYNMMKTNTAVRPYCFIEFDNFIQ

	RN	NFISSLGVS YMMMLCTENYPNVLA FSFLDELQKEFITTYNMMKTNTAVRPYCFIEFDNFIQ
	HP	RTKQRYNNPRSLSTKINLSDMQTEIKLRPPYQISMCELGSANGVTSAFSVDCKGAGKISS
		*****.*****.*****
25	RN	RTKQRYNNPRSLSTKINLSDMQMEIKLRPPYQIPMCELGSANGVTSAFSVDCKGAGKISS
	HP	AHQRLPATLSGIVGFILSLLCGALNLIRGFHAIESLLQSDGDDFNYYIAFFLGTAACLY
		*****.*****.***.*****
	RN	AHQRLPATLSGIVAFILSLLCGALNLIRGFHAIESLLQSDGEDFSYIMIAFFLGTAACLY
	HP	QCYLLVYYTGWRNVKSFLTFLGLICLCNMYLYELRNWLQLFHVTVGAFVTLQIWL RQAQG
30		*
	RN	QMICLCLQGRKERT

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA421925) in ESTs, but, since they
5 are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP01956> (SEQ ID Nos. 62, 72, and 82)

10 Determination of the whole base sequence of the cDNA insert of clone HP01956 obtained from cDNA library of human liver revealed the structure consisting of a 86-bp 5'-untranslated region, a 552-bp ORF, and a 359-bp 3'-untranslated region. The ORF codes for a protein consisting
15 of 183 amino acid residues and there existed one putative transmembrane domain. Figure 22 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product
20 of 20.5 kDa that was almost identical with the molecular weight of 20,073 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the yeast hypothetical protein 21.5
25 kDa (SWISS-PROT Accession No. P53073). Table 15 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the yeast hypothetical protein 21.5 kDa (SC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that
30 of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology

of 34.3% in the C-terminal region of 108 amino acid residues.

Table 15

5	HP MTAQGGLVANRGRFRKWAIELSGPGGSRGRSDRSGQGDSLVPVGYLDKQVPDTS
	SC MSEQEPYEWAKHLLDTKYIEKYNIQNSNTLPSPPGFEGNSSKGNVTRKQQDATSQTTSLA
	HP VQETDRILVEKRCWDIALGPLKQIPMNLFIMYMAGNTISIFPTMMVCMMAWRPIQALMAI
	.* .. *.*.* * * *.*.*.* *.*.*.* *.*.* *.* *.*.*.*
10	SC QKNQITVLQVQKAWQIALQPAKSIPMNIFMSYMSGTSLQIIPIMTALMLLSGPIKAIFST
	HP SATFK--MLESSSQKFLQGLVYLIGNLMGLALAV-Y-KCQSMGLLPTHASDWLAFIEPPE
	*** * ..**.*.* *.* *.* *.* *.* *.* *.* *.* *.*
	SC RSAFKPVLGNKATQSQVQTAMFMYIVFQGVLMYIGYRKLNSMGLIPNAKGDWLPWERIAH
	HP RMEFSGGGLLL
15	SC YNNGLQWFSD

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA159753) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02545> (SEQ ID Nos. 63, 73, and 83)

Determination of the whole base sequence of the cDNA insert of clone HP02545 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 133-bp 5'-untranslated region, a 984-bp ORF, and a 636-bp 3'-untranslated region. The ORF codes for a

protein consisting of 327 amino acid residues and there
existed a putative secretory signal at the N-terminus and
one putative transmembrane domain at the C-terminus. Figure
23 depicts the hydrophobicity/hydrophilicity profile,
5 obtained by the Kyte-Doolittle method, of the present
protein.

The search of the protein data base using the amino
acid sequence of the present protein revealed that the
protein was similar to the rat embigin (EMBL Accession No.
10 AJ009698). Table 16 shows the comparison between amino acid
sequences of the human protein of the present invention (HP)
and the rat embigin (RN). Therein, the marks of -, *, and .
represent a gap, an amino acid residue identical with that
of the protein of the present invention, and an amino acid
15 residue similar to that of the protein of the present
invention, respectively. The both proteins shared a homology
of 65.4% in the entire region.

Table 16

```

HP MRALPGLLEARARTPRLLLLQCLLAAARPSSADGSAPDSPFTSPPLREEIMAN--NFSLE
  ** . ** . * . . ***** . ***** . * . . . . ***** . ***** . * . **
5 RN MRSHTGLRALVAPGCSLLLL-YLLAATRPDRAVGDPADSAFTSLPVREEMMAKYANLSLE
HP SHNISLTEHSSMPVEKNITLERPSNVNLTCQFTTSGDLNAVNVTWKKDGEQLE--NNYLV
  . ***** . . . . * . ***** . . . . * . ***** . . . . * . . . .
RN TYNISLTEQTRVS-EQNITLERPSHLELECTFTATEDVMSMNVTWKKDDALLETTDGFNT
HP SATGSTLYTQYRFTIINSKQMGSYSCFFREEKEQRGTFNFKVPELHGKNKPLISYVGDST
10 . * . ***** . ***** . ***** . ** ***** . * . ***** . *****
RN TKMGDTLYSQYRFTVFNSKQMGKYSCFLGEE--LRGTFNIRVPKVHKGKNKPLITYVGDST
HP VLTCKCQNCFPLNWTWYSSNGSVKVPVGVQM-NKYVINGTYANETKLKITQILLEEDGESY
  * . * . ***** . ***** * . . . . * . . . * . * . ***** . ***** . *
RN VLKCECQNCPLNWTWYMSNGTAQVPIDVHVNDKFDINGSYANETKLKVHLLLEEDGGSY
15 HP WCRALFQLGESEEHIELVVLVLSYLVPLKPFVIVAIEVILLVATILLCEKYTQKKKKHSDEG
  ***** * . ***** . ***** . ***** . ***** . ***** . ***** . *
RN WCRAAFPLGESEEHKLVVLSFMVPLKPFVIAIEVILLVATILLCEVYTQKKKNPDDG
HP KEFEQIEQLKSDDSDNGIENNVPRHRKNESLGQ
  ***** . ***** . * . . * . *
20 RN KEFEQIEQLKSDDSDNGIENNVPRYRKTDSDGQ

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Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA312629) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02551> (SEQ ID Nos. 64, 74, and 84)

Determination of the whole base sequence of the cDNA insert of clone HP02551 obtained from cDNA library of human

osteosarcoma cell line Saos-2 revealed the structure consisting of a 61-bp 5'-untranslated region, a 672-bp ORF, and a 384-bp 3'-untranslated region. The ORF codes for a protein consisting of 223 amino acid residues and there
5 existed a putative secretory signal at the N-terminus. Figure 24 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was somewhat larger than
10 the molecular weight of 24,555 predicted from the ORF. In this case, the addition of a microsomal led to the formation of a product of 26 kDa from which the secretory signal is considered to have been cleaved. Application of the (-3,-1) rule, a method for predicting the cleavage site of the
15 secretory signal sequence, allows to expect that the mature protein starts from glutamine at position 20.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse FGF binding protein
20 (GenBank Accession No. U49641). Table 17 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse FGF binding protein (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the
25 protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 21.2% in the entire region other than the N-terminal region. In particular, all the eight cysteine residues contained in the
30 both proteins were conserved.

Table 17

```

HP                                     MKFVPCLLLVTLSCGLTGLQAPRQKQGST
                                     ...**..*...
5  MM MRLHSLILLSFLLLATQAFSEKVRKRAKNAPHSTAEEGVEGSAPSLGKAQNQRSRTSKS
HP  GEEFHFQTGGRDSCMRPSSLGQGAGEVWLRVDCRNTDQTYWCEYRGQPSMCQAFADPK
    ..* * .....* .....*...*...*...*...*...*...*...*...
MM  LTHGKFVTKDQATC---RWAVTEEEQGISLKVQCTQADQEFSCVFAGDPTDCLKHDKD-Q
HP  SYWNQALQELRRLHHACQGA-PVLRPSVCREAGPQAHMQQVTSSLKGSPEPNQQPEAGTP
10 ***..**..*...*...*...*...*...*...*...*...*...*...
MM  IYWKQVARTLRKQKNICRDAKSVLKTRVCRKRFPESNLKLVPNPARGNTKPRKEKAEVSA
HP  SLRPKATVKLTEATQLGKDSMEELGKAKPTTRPTAKPTQPGPRPGGNEEAKKKAWEHWCW
    ..* .....*...*...*...*...*...*...*...*...*...
MM  REHNKVQEA VSTEPNRIKEDI-TLNPAATQTM-TIRDPECLEDPDVLNQ-RKTALEFCGE
15 HP  PFQALCAFLISFFRG
    ..*...*.....
MM  SWSSICTFFLNMLQATSC

```

20 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. AA317400) in ESTs, but, since they
are partial sequences, it can not be judged whether or not
25 any of these sequences codes for the same protein as the
protein of the present invention.

<HP02631> (SEQ ID Nos. 65, 75, and 85)

30 Determination of the whole base sequence of the cDNA
insert of clone HP02631 obtained from cDNA library of human
osteosarcoma cell line Saos-2 revealed the structure
consisting of a 42-bp 5'-untranslated region, a 147-bp ORF,

and a 1191-bp 3'-untranslated region. The ORF codes for a protein consisting of 48 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 25 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa or less.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA156969) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02632> (SEQ ID Nos. 66, 76, and 86)

Determination of the whole base sequence of the cDNA insert of clone HP02632 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 50-bp 5'-untranslated region, a 1116-bp ORF, and a 337-bp 3'-untranslated region. The ORF codes for a protein consisting of 371 amino acid residues and there existed eight putative transmembrane domains. Figure 26 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein CELC2H12 (GenBank Accession No. U23169). Table 18 shows the comparison between amino acid sequences

of the human protein of the present invention (HP) and the C. elegans hypothetical protein CELC2H12 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 51.4% in the entire region.

Table 18

10

HP MAWTKYQLFLAGLMLVTGSINTLSAKWADNFMAEGCGGSKEHSFQHPFLQAVGMFLGEFS
*.****.*.*.....*.....*.....*

CE MVAFAV IISVMMVVTGSLNTICAKWADSIKAD-----GVPFNHPFLOATCMFFGEFL

15

HP CLAAFYL-----LRCRAAGQSDS-----SVDPQQPFNPLLFLPPALCDMTGTSL

** . . * . * * . . . * . * . * . . . ***** . ** . ***** . ****

CE CLVVFFLI FG YKRYVWNRANVQGESGSVTEITSEEKPTLPPFNPFLLFFPPALCDILGTSI

HP MYVALNMTSASSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWLGI LATIAGLVVVGLADLL

** . . ** . * . ***** . ** . . * * . * . * . . *** . ** . *

20

CE MYIGLNLTASSFQMLRGAVIIFTGLLSVGMLNAQIKPFWFGMLFVMLGLVIVGVTDIY

HP SKHDSQHKLSEVITGDLLIIMAQIIVAIQMVLEEKFFVYKHNHPLRAVGTEGLFGFVILS

..*.. .. ***.***.***** *.*. *.*. * * * * *.**

CE YDDDPLDDKNAIITGNLLIVMAQIIIVAIQMVYEQKYLTKYDVPALFAVGLEGLFGMVTLT

HP LLLVPMYYIPAG-SFSGNPRGTLEDALDAFCQVGQOPLIAVALLGNISSIAFFNFAGISV

. * . . * . * * * . . . * * . * * * * * * . . * * * * . * * * . . * * * * * * * * * . * *

25

CE ILMIPFYIHPRTFSTNPEGRLEDVFYAWKEITEPTIALALSGTVVSIAFFNFAGVSV

HP TKELSATTRMVLDSLRTVVIIWALSLALGWEAFHALQILGFLILLIGTALYNGLHRPLLGR

*****. ** . *** . * . * * * * . * . ** . * . . ** . ** . .

CE TKELSATTRMVLDSVRTLVIVVSIPLFHEKFIAIQLSGFAMLILGTLIYNDILIGPWR

HP LSRGRPLAEESQERLLGGTRTPINDAS

30

CE RNILPNLSSHANCARCWLCICGGDSELIEYEQEDOEHLMEA

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N50907) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10488> (SEQ ID Nos. 67, 77, and 87)

Determination of the whole base sequence of the cDNA insert of clone HP10488 obtained from cDNA library of human liver revealed the structure consisting of a 39-bp 5'-untranslated region, a 273-bp ORF, and a 421-bp 3'-untranslated region. The ORF codes for a protein consisting of 90 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 27 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa that was almost identical with the molecular weight of 10,151 predicted from the ORF. When expressed in COS7 cells, an expression product of about 6 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H73534) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10538> (SEQ ID Nos. 68, 78, and 88)

Determination of the whole base sequence of the cDNA insert of clone HP10538 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 357-bp 5'-untranslated region, a 1500-bp ORF, and a 1911-bp 3'-untranslated region. The ORF codes for a protein consisting of 499 amino acid residues and there existed at least four putative transmembrane domains. Figure 28 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse pore-forming K⁺ channel subunit (GenBank Accession No. AF056492). Table 19 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse pore-forming K⁺ channel subunit (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 32.4% in the N-terminal region of 241 amino acid residues.

Table 19

```

HP  MVDRGPLLLTSAIIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLKEFPCLGQEGLDK
      * . . . . . * . * . . . . . * . . . . . * . . . . . * . . . . .
5  MM  MRSTLLALLLVLLYLVS GALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED
HP  ILEVVS DAAGQG-----VAITGNQTFNWNWPNAMIFAATVITTIGYGNVAPKTPAGRIF
      . . . . . * * * . . . . . * . * . . . . . * . . . . . * . . . . .
MM  FIKLLVEALGGGANPETS WTNSSNHSSAWNLSGAFFFSGTIITTIGYGNIVLHTDAGRIF
HP  CVFYGLFGVPLCLTWISALGKFFGGRAKR----LGQFLTKRGVSLRKAQITCTVIFIVWG
10  * . . . . * . . . . . * . . . . . * . . . . . * . . . . . * . . . . .
MM  CIFYALVGIPFLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLLIG
HP  VLVHLVIPPFVFMVTEGWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVELW
      * . . . . * . . . . . * . . . . . * . . . . . * . . . . . * . . . . .
MM  CLLFVLTPFTVFSYME SWSKLEAIYFVIVTLTTVGF GDYVPG-DGTGQNSPAYQPLVWF
15  HP  IYLG L WLSLFVNWKVSMFVEVHKAIKRRRRRRKESFESSPHSRKALQVKGSTASKDVNI
      * . . . . .
MM  ILFGLAYFASVLT TIGNWLRAVSRRTAEMGGLTAQAASWTGTVTARVTQRTGPSAPPPE

```

20 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. R25184) in ESTs, but, since they are
partial sequences, it can not be judged whether or not any
25 of these sequences codes for the same protein as the protein
of the present invention.

<HP10542> (SEQ ID Nos. 69, 79, and 89)

30 Determination of the whole base sequence of the cDNA
insert of clone HP10542 obtained from cDNA library of human
stomach cancer revealed the structure consisting of a 23-bp
5'-untranslated region, a 321-bp ORF, and a 426-bp 3'-

untranslated region. The ORF codes for a protein consisting of 106 amino acid residues and there existed one putative transmembrane domain. Figure 29 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 11,724 predicted from the ORF. When expressed in COS7 cells, an expression product of about 13 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA029683) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10571> (SEQ ID Nos. 70, 80, and 90)

Determination of the whole base sequence of the cDNA insert of clone HP10571 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 95-bp 5'-untranslated region, a 459-bp ORF, and a 675-bp 3'-untranslated region. The ORF codes for a protein consisting of 152 amino acid residues and there existed one putative transmembrane domain. Figure 30 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 20 kDa that was larger than the molecular weight of 17,062 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 23 kDa

which is considered to have a sugar chain being attached after secretion. In addition, there exists in the amino acid sequence of this protein one site at which N-glycosylation may occur (Asn-Ile-Thr at position 10).

5 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA105822) in ESTs, but, since they are partial sequences, it can not be judged whether or not
10 any of these sequences codes for the same protein as the protein of the present invention.

<HP01470> (SEQ ID Nos. 91, 101, and 111)

15 Determination of the whole base sequence of the cDNA insert of clone HP01470 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 157-bp 5'-untranslated region, a 1077-bp ORF, and a 385-bp 3'-untranslated region. The ORF codes for a protein consisting of 358 amino acid residues and there existed one putative
20 transmembrane domain. Figure 31 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 43 kDa that was somewhat larger than the molecular weight
25 of 40,489 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 40 kDa from which the secretory signal is considered to have been cleaved and a product of 43.5 kDa which is considered to have been subjected to some modification. Application of the
30 (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glycine at position 23. When

expressed in COS7 cells, an expression product of about 44 kDa was observed in the supernatant fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein 39.9 kDa (SWISS-PROT Accession No. Q10005). Table 20 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein 39.9 kDa (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 58.9% in the entire region.

Table 20

[illegible]

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA282838) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

30 <HP002419> (SEQ ID Nos. 92, 102, and 112)

Determination of the whole base sequence of the cDNA insert of clone HP02419 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 253-bp

5'-untranslated region, a 681-bp ORF, and a 1120-bp 3'-untranslated region. The ORF codes for a protein consisting of 226 amino acid residues and there existed four putative transmembrane domains. Figure 32 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human hypothetical protein KIAA0108 (SWISS-PROT Accession No. Q15012). Table 21 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human hypothetical protein KIAA0108 (KI). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 43.9% in the entire region.

of the translation product and the sequence comparison data with the *Caenorhabditis elegans* homologue. The ORF codes for a protein consisting of 195 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the intermediate region. Figure 33 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 58 kDa. In this case, the addition of a microsome led to the formation of a product of 56 kDa from which the secretory signal is considered to have been cleaved. Since both of these products are larger than the molecular weight of 22 kDa predicted from the ORF, it is likely that the protein interacts with another protein.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein C35C5.3 (EMBL Accession No. Z78417). Table 22 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein C35C5.3 (CE). U at position 49 in the amino acid sequence of the protein of the present invention represents selenocysteine. Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 37.9% in the entire region other than the N-terminal region. Cystein was found in the sequence of the *C. elegans* protein at the position corresponding to position 49 encoded by the stop codon (selenocysteine) of the protein of the present invention.

Table 22

	HP		MRLLLL
--	----	--	--------

5	CE MRIHDELQKQDMSRFGVFIIGVLEFFMSVCDVLRTEESHSHDENHVHEKDDFEAEFGDETDS		
	HP LLVAASAMVRSEASANLGGVPSKRLKMQYATGPLLKQICVSUGYRRVFEEYMRVISQRY		
		* *.. *** **.....
	CE QSFSQGTEEDHIEVREQSSFVKPTAVHHAKDLPTLRIFYCVSCGYKQAFDQFTTFAKEY		
	HP PDIRIEGENYLPQPIYRHIAFSLSVFKLVLIIGLIIVGKDPFAFFGMQAPSIWQWGQENKV		
10	*...***.*. * ..* ** *.... *.. * .***. **. * * *		
	CE PNMPIEGANFAPVLWKAYVAQALSFKMAVLVLVLGGINPFERFGLGYPQILQHAHGNKM		
	HP YACMMVFFLSNMIENQCMSTGAFEITLNDVPVWSKLESGLPSMQQLVQILDNEMKLNKH		
		.***.*.*..... .*****. *.. .*****.*.* *	
	CE SSCMLVFMLGNLVEQSLISTGAFEVYLGNEQIWSKIESGRVPSPQEFMQLIDAQLAVLGK		
15	HP MDSIPHHR		
	CE APVNTESFGEFQQT		

20 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA156969) in ESTs, but, since they are partial sequences, it can not be judged whether or not

25 any of these sequences codes for the same protein as the protein of the present invention.

<HP02695> (SEQ ID Nos. 94, 104, and 114)

30 Determination of the whole base sequence of the cDNA insert of clone HP02695 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 112-bp 5'-untranslated region, a 1020-bp ORF, and a 160-bp 3'-

untranslated region. The ORF codes for a protein consisting of 339 amino acid residues and there existed three putative transmembrane domains. Figure 34 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 38 kDa that was almost identical with the molecular weight of 38,274 kDa predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the rat hypertension-induced protein S-2 fragment (PIR Accession No. 539959). Table 23 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the rat hypertension-induced protein S-2 fragment (RN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 74.3% in the entire region.

Table 23

HP MNWELLLWLLVLCALLLLLVQLLRFLRADGDLTLLWAEWQGRRPEWELTDMVVWVTGASS

5 HP GIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPLDLTDTGSHEA
 *****.***.***.
 RN VKRRSLENGNLKEKDILVLPLDLADTSSHDI
 HP ATKAVLQEFGRIDILVNNGGMSQRSCLMDTSLDVYRKLIENYLGTVSLTKCVLPHMIER
 .**... ** .*...***.***** ****.*

10 RN ATKTVLQEFGRIDILVNNGGVAHASLVENTNMDIFKVLIEVNYLGTVSLTKCFLPHMMER
 HP KQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGPVQSN
 .*****.*
 RN NQGKIVVMKS

15

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T84331) in ESTs, but, since they are

20 partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

25

<HP10031> (SEQ ID Nos. 95, 105, and 115)

Determination of the whole base sequence of the cDNA insert of clone HP10031 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 55-bp 5'-untranslated region, a 1464-bp ORF, and a 649-bp 3'-untranslated region. The ORF codes for a

30 protein consisting of 487 amino acid residues and there existed eleven putative transmembrane domains. Figure 35 depicts the hydrophobicity/hydrophilicity profile, obtained

by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight. When expressed in COS7 cells, an expression product of about 55 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein CELK07H8 (GenBank Accession No. AF047659). Table 24 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein CELK07H8 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 44.2% in the entire region.

Table 24

HP MDGTETRQRRLDSCGKPGELGLPHPLSTGGLPVAS

5 CE MKGGGGIGDGKKDYQSAVHEGLTTFDQLGIALEDVGKSMDEATATPGGSLFSRVIFRFRN
HP EDGALRAPESQSVTPKPLETEPSRETAWSIGLQVTVPFMFAGLGLSWAGMLLDYFQHPV
...... . . . *... . ** ** ***** .***... **
CE ENSSLKSRTYDHSNDLVNMSVIPAESSYVLFFQVLFFFAVAGLGMVFAVLVLSIVVTWPL
HP FVEVKDLLTLVPPLVGLKGNLEMTLASRLSTAANTGQIDDPQEQHRVISSNLALIQVQAT
10 * * . .*.****.*.*****.***** ** *..*..... *. *****.*****
CE FEEIPEILILVPALLGLKGNLEMTLASRLSTLANLGHMDSSKQRKDVVIANLALVQVQAT
HP VVGLLAAVAALLLGVVSREEVDVAKVELLCASSVLTAFLAAAFALGVLVCIVIGARKLGV
.... * *. * *. *.*****. ** *...*..***** ..
CE VVAFLASAFAAALAFIPSGDFDWAHGALMCASSLATAACSASLVLSLLMVVVIVTSRKYNI
15 HP NPDNIATPIAASLGDLITLSILALVSSFFYR-HKDSRYLTPLVCLSF AALTPVWVLI AQ
****.*****.***..**.. * * . *.....* . * . * * * * . **..
CE NPDNVATPIAASLGDLTTLTVLAFFGSVFLKAHNTESWLVNIVIVLFLLLLFPWIKIANE
HP SPPIVKILKFGWFPIILAMVISSFGGLILSKTVSKQQYKGMAIFTPVICGVGGNLVAIQT
 . . . * ** *.*****.*****.*******..*****.***..
20 CE NEGTOETLYNGWTPVIMSMLISSAGGFILETAV--RRYHSLSTYGPVLNGVGGNLAAVQA
HP SRISTYLHMWSAPGVLP LQ--MKKFWPNPCSTFCTSEINSMSARVLLLLLVVPGHLIF-FY
....* . . ****** . . . * ..* ..* ..*.....*****. * *
CE SRLSTYFHKAGTVGVLPNEWTVSRF-TSVQRAFFSKEWDSRSARVLLLLLVVPGHICFNFL
HP I-IYLVEGQSVINSQ--TFVVLYLLAGLIQVTILLYLAEVMVRLTWHQALDPDNHCIPYL
25 * *..**..*.....*****.* * *. ***** *****
CE IQLFTLTSKNNVTPHGPLFTSLYMIAAIIQVVILLFVCQLLVALLWKWKIDPDNSVIPYL
HP TGLGDL LGTGLLALCFFTDWLLKSKAELGGISELASGPP
*.*****. . *.*
CE TALGDL LGTGLLFIVFLTDDHFDPKELTSS

30

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for

example, Accession No. AA334000) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

5

<HP10530> (SEQ ID Nos. 96, 106, and 116)

Determination of the whole base sequence of the cDNA insert of clone HP10530 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure
10 consisting of a 80-bp 5'-untranslated region, a 1182-bp ORF, and a 95-bp 3'-untranslated region. The ORF codes for a protein consisting of 393 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 36 depicts the hydrophobicity/hydrophilicity profile,
15 obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 46 kDa that was somewhat larger than the molecular weight of 44,912 predicted from the ORF. In this case, the addition of a microsome led to the formation
20 of a product of 45.5 kDa from which the secretory signal is considered to have been cleaved. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from lysine at position 23. When expressed in
25 COS7 cells, an expression product of about 43 kDa was observed in the supernatant fraction and the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the
30 protein was similar to the Arabidopsis thaliana hypothetical protein IG002N01 (GenBank Accession No. AF007269). Table 25 shows the comparison between amino acid sequences of the

human protein of the present invention (HP) and the A.
thaliana hypothetical protein IG002N01 (AT). Therein, the
marks of -, *, and . represent a gap, an amino acid residue
identical with that of the protein of the present invention,
5 and an amino acid residue similar to that of the protein of
the present invention, respectively. The both proteins
shared a homology of 27.0% in the N-terminal region of 355
amino acid residues.

Table 25

HP	MRTLFLNLLWL
5	AT MELTSFQKSPSSNDVVSFSVSLVRNSMARRRRSSAAESLKRRNDGYESLCQVVQQDSDRR HP ALACSPVHTTLSKSDAKKAASKTLEKSQFSDKPVQDRGLVVTDLKAESVVLEHRSYCSA*. * **.. *... ..
10	AT LITIFVIFVIVIPAVSIAVYKVKFADRVIQTESSIRQKGIVKTDINFQEILTEHSK--AS HP KARDRHFAGDVLGYVTPWNSHGYDVTKVFGSKFTQISPVLQ-LKRRGREMF EVTGLHDV*... **..*... ..*... ..*... *...*... ..*... AT ENSTRHYDYPVLAYITP--CQGSGL--VLEGR-HNADKGWIQELRSRGNALSASKGLPKL HP DQGWMAVRKHAKGLHIVPRLLFEDWTYDDFRNVLDSEDEIEELSKTVVQVAKNQHFDFG * * . ** ..*... *...
15	AT ---YNSCIFHALKRMNFFTLELVNFNTYLVIMFALNS-REMEYNGIVLESWSRWAAYGVL HP VVEVWNQLLSQKRVGLIHMLTHLAEALHQARLLALLVIPPAITPGTDQLGMFTHKEFEQL * . * * . *... ..* AT HDPDLRKMALKFVKQLGDALHSTSSPRNNQOHMQFMYVVGPPRSEKLQMYDFGPEDLQFL HP APVLDGFSMLTYDYSTAHPGPNAPLSWVRACVQ-VLDPKSK---WRSKILLGLNFYGM .*****.*...*****... ..*... ..*...*****
20	AT KDSVDGFSMLTYDFSNPQNP GP NAPVKWIDLTCLKLLGSSNNIDSNIARKVLLGINFYGN HP DYATSKDAREPVVGARYIQTLKDHPRMVWDSQASEHFF EYKKSRSRGRHVVFYPTLKS LQ *...* ..*...* *...*...* ..*...*...* *... ..*...*...* AT DFVISGGGGGAITGRDY LALLQKHKPTFRWDKESGEHLFMYRDDKNIKHAVFYPTLMSIL HP VRLELARELGVGVS IWELGQGLDYFYDLL
25	.*** ** *.*****.*...* AT LRLENARLWGIGISIWELGQDKGHFGKYAEASLEASSIFSGHTFDMQFRTNPRQLSRNGS

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA302913) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the

protein of the present invention.

<HP10541> (SEQ ID Nos. 97, 107, and 117)

Determination of the whole base sequence of the cDNA
5 insert of clone HP10541 obtained from cDNA library of human
stomach cancer revealed the structure consisting of a 7-bp
5'-untranslated region, a 591-bp ORF, and a 113-bp 3'-
untranslated region. The ORF codes for a protein consisting
of 196 amino acid residues and there existed a putative
10 secretory signal at the N-terminus. Figure 37 depicts the
hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
of 23 kDa that was somewhat larger than the molecular weight
15 of 21,553 predicted from the ORF. In this case, the addition
of a microsome led to the formation of a product of 20 kDa
from which the secretory signal is considered to have been
cleaved and a product of 23 kDa which is considered to have
a sugar chain being attached. Application of the (-3,-1)
20 rule, a method for predicting the cleavage site of the
secretory signal sequence, allows to expect that the mature
protein starts from glycine at position 41. In addition,
there exists in the amino acid sequence of this protein one
site at which N-glycosylation may occur (Asn-Leu-Thr at
25 position 185).

The search of the protein data base using the amino
acid sequence of the present protein revealed that the
protein was similar to the human zymogen membrane protein
(GenBank Accession No. AF056492). Table 26 shows the
30 comparison between amino acid sequences of the human protein
of the present invention (HP) and the human zymogen membrane
protein (ZM). Therein, the marks of -, *, and . represent a

gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 37.6% in the C-terminal region of 133 amino acid residues.

Table 26

10	HP MWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFS-TTEDYD	**.***** ** *
	ZM MLTVALLALLCASASGNAIQARSSSYSGEYGS GGGKRF SHSGNQLD	
	HP HEITGLRVS VGLLLVKSVQVKLGDSWDVKLGALGGNTQEVTLQPG EYITKV FVAFQAFLR	
		.**.*. *. *. .*. .*. .*. *.******
	ZM GPITALRVRVNTYYIVGLQVRYGKVWSDYVGG RNGDLEE IFLHPGESVIQVSGKYK WYLK	
15	HP GMVMYTSKDRYFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWN-YPLEEP	
		..* .*.****. *** .* .* * . . ** * *. * ..*****. **
	ZM KLVFVTDKGRYLSFGKDSGTSFNAVPLHPNTVLRFISGRSGSL-IDAIGLHWDVYPTSCS	
	HP TTEPPVNLTYSANSPVGR	
20	ZM RC	

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA340605) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

30

<HP10550> (SEQ ID Nos. 98, 108, and 118)

Determination of the whole base sequence of the cDNA

insert of clone HP10550 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 241-bp 5'-untranslated region, a 324-bp ORF, and a 86-bp 3'-untranslated region. The ORF codes for a protein consisting of 107 amino acid residues and there existed one putative transmembrane domain. Figure 38 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA348310) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10590> (SEQ ID Nos. 99, 109, and 119)

Determination of the whole base sequence of the cDNA insert of clone HP10590 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 77-bp 5'-untranslated region, a 1053-bp ORF, and a 180-bp 3'-untranslated region. The ORF codes for a protein consisting of 350 amino acid residues and there existed one putative transmembrane domain. Figure 39 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 40 kDa that was almost identical with the molecular weight of 39,285 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of

43 kDa which is considered to have a sugar chain being attached. In addition, there exist in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Asn-Ser at position 144 and Asn-Leu-Thr at position 328).

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA461346) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10591> (SEQ ID Nos. 100, 110, and 120)

Determination of the whole base sequence of the cDNA insert of clone HP10591 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 232-bp 5'-untranslated region, a 324-bp ORF, and a 844-bp 3'-untranslated region. The ORF codes for a protein consisting of 107 amino acid residues and there existed one putative transmembrane domain. Figure 40 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 11,328 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H09424) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein

of the present invention.

<HP01462> (SEQ ID Nos. 121, 131, and 141)

Determination of the whole base sequence of the cDNA
5 insert of clone HP01462 obtained from cDNA library of human
fibrosarcoma cell line HT-1080 revealed the structure
consisting of a 121-bp 5'-untranslated region, a 1452-bp ORF,
and a 477-bp 3'-untranslated region. The ORF codes for a
protein consisting of 483 amino acid residues and there
10 existed a putative secretory signal at the N-terminus.
Figure 41 depicts the hydrophobicity/hydrophilicity profile,
obtained by the Kyte-Doolittle method, of the present
protein. In vitro translation resulted in formation of a
translation product of 72 kDa that was larger than the
15 molecular weight of 55,838 predicted from the ORF.
Application of the (-3,-1) rule, a method for predicting the
cleavage site of the secretory signal sequence, allows to
expect that the mature protein starts from lysine at
position 21.

20 The search of the protein data base using the amino
acid sequence of the present protein revealed that the
protein was similar to the *Caenorhabditis elegans*
hypothetical protein ZK1058.4 (EMBL Accession No. Z35604).
Table 27 shows the comparison between amino acid sequences
25 of the human protein of the present invention (HP) and the *C.*
elegans hypothetical protein ZK1058.4 (CE). Therein, the
marks of -, *, and . represent a gap, an amino acid residue
identical with that of the protein of the present invention,
and an amino acid residue similar to that of the protein of
30 the present invention, respectively. The both proteins
shared a homology of 35.6% in the entire region.

Table 27

HP MKAFHTFCVLLVFGSVSEAKFDDFEDEEDIVEYDDNDFAEFEDVMEDSVTESPQVVIIT
* *

5 CE MKIVWIFLIFFIGFAIST

HP EDDE-DETTVELEGQDENQEGDFEDADTQEGDTESEPYDDEEFEGYEDKP-----D
* *

HP DDNEFAEFEDFEVGGSSATQAPEIQREGEPPVLKQKDDFEEDFGVVVEEPEEAEKVREAD
* *

HP TSSSKNKDPITIVDVPAPHLQNSWESYYLEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNT
* *

10 HP SDDAAPAQPLKFADVPAHFRSNWASYQVEGIVVLIILYMTNYLIGKTTNASIAQTIFDM
* *

HP HRELLESNFTLVGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCGMLIQLRFLKRQDL
* *

CE CRPTLEEQFAVVGDDGTTDLDKMIPSLKHDTSTFSAWCTGRVNVNSLFLQMKMVKRQDV
* *

15 HP LNVLARMMRPVSDQVQIKVTMN-DEDMDTYVFAVGTRKALVRLQKEMQDLSEFCSDKPKS
* *

CE VSRIMEMFTPSGDKMTIKASLETTNDTDPLIFAVGEKKIASKYFKEMLDLNSFASERKQA
* *

HP GAKYGLPDSLAILSEMGEVTDGMMDTKMVHFLTHYADKIESVHFSDQFSGPKIMQEEGQP
* *

20 CE AQQFNLPASWQVYADQNEVVFSILDPGVVSLKKHEDAIEFIHISDQFTGPKPAEGESYT
* *

HP LKLPDTRKRTLLFTFNVPVSGNTYPKDMEALLPLNMVIYSIDKAKKFRNLNREGKQKADKN
* *

CE -RLPEAQRYMFVSLNLQYLG---QDEESVMEILNLVLYLIDKARKMKLSKDAKVAERR
* *

HP RARVEENFLKLTHVQRQEAQAQSRREEKKRAEKERIMNEEDPEKQRRLEEAALRREQKLE
* *

25 HP RKEFEDAFLKQTHQFRQEAQAARREEKTRERKQKLMDSDPERQKRLEAKELKREKA--
* *

HP KKQMKMKQIKVKAM
* *

CE -KSPKMKQLKVK

30

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for

example, Accession No. AA307793) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

5

<HP02485> (SEQ ID Nos. 122, 132, and 142)

Determination of the whole base sequence of the cDNA insert of clone HP02485 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 69-bp
10 5'-untranslated region, a 1005-bp ORF, and a 1672-bp 3'-untranslated region. The ORF codes for a protein consisting of 334 amino acid residues and there existed one putative transmembrane domain. Figure 42 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-
15 Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 36 kDa that was almost identical with the molecular weight of 38,171 predicted from the ORF. When expressed in COS7 cells, an expression product of about 23 kDa was
20 observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein W01A11.2 (GenBank Accession No. U64852).
25 Table 28 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein W01A11.2 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of
30 the present invention, respectively. The both proteins shared a homology of 45.5% in the entire region.

insert of clone HP02798 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 31-bp 5'-untranslated region, a 804-bp ORF, and a 301-bp 3'-untranslated region. The ORF codes for a
5 protein consisting of 267 amino acid residues and there existed four putative transmembrane domains. Figure 43 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation
10 product of 29 kDa that was almost identical with the molecular weight of 30,778 predicted from the ORF. When expressed in COS7 cells, an expression product of about 26 kDa was observed in the membrane fraction.

The search of the protein data base using the amino
15 acid sequence of the present protein revealed that the protein was similar to the human DHHC-containing cysteine-rich protein (GenBank Accession No. U90653). Table 29 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human DHHC-containing cysteine-rich protein (DH). Therein, the marks of
20 -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a
25 homology of 35.0% in the intermediate region of 100 amino acid residues. The positions of seven cysteines were conserved between the two proteins. The protein of the present invention also had the DHHC (Asp-His-His-Cys) sequence.

Table 29

HP	MAPWALLSPGVLVRTGHTVLTWGI
5	DH MYKMNICNKPSNKTAPKSVWTAPAQPSGSPPELQQRSSRRNGWSWPPHPLQIVAWLLYL HP TLVFLFLHDTLQWEEQGEELLPLTFLLLVLGSLLLYLAVSLMDPGYVNVQPP-QEELK * * * *
10	DH FFAVIGFGILVPLLPHHWVPAGYACMGAIFAGHLVVHLTAVSIDPADDNVRDKSYAGPLP HP EEQTAMVPPAIPLRRCRYCLVLQPLRARHCRECRRCVRRYDHHCPWMENCVGERNHPLFV * * * * * * DH IFNRSQHAHVIEDLHCNLCNVDVSARSKHCSACNKCVCGFDDHCKWLNNCVGERNYRFL HP VYLALQLVLLWGLYLAWSGLRFFQPWGLWLRSSGLLFATFLLLSLFSLVASLLLVSHLY . * . * . *
15	DH HSVASALLGVLLLVLGGHICLRGVLCQPHASAHQPTL

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. D79050) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

25 <HP10041> (SEQ ID Nos. 124, 134, and 144)

Determination of the whole base sequence of the cDNA insert of clone HP10041 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 12-bp 5'-untranslated region, a 321-bp ORF, and a 286-bp 3'-untranslated region. The ORF codes for a protein consisting of 106 amino acid residues and there existed one putative transmembrane domain. Figure 44 depicts

the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 12,060 predicted from the ORF. When expressed in COS7 cells, an expression product of about 13 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein K10B2.4 (GenBank Accession No. U28730). Table 30 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein K10B2.4 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 62.1% in the entire region.

Table 30

HP	MSTNNMSDPRRPKNKVLRYKP---PPSECNPALDDPTPDYMNLLGMIFSMCGLMLKLKWCA
	.****.*...****
CE	MQQNGDPRRTNRIVRYKPLDSTANQQQAISEDPLPEYMNVLGMIFSMCGLMIRMKWCS
HP	WVAVYCSFISFANSRSEDTKQMMSSFMLSISAVVMSYLQNPQPMTPPW
	.. ** *****.*.*.*.*.*****.***** *..***
CE	WLALVCSCISFANTRTSDDAKQIVSSFMLSISAVVMSYLQNPSPPIPPWVTLQ

Furthermore, the search of the GenBank using the base

sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H20098) in ESTs, but, since they are partial sequences, it can not be judged whether or not any
5 of these sequences codes for the same protein as the protein of the present invention.

<HP10246> (SEQ ID Nos. 125, 135, and 145)

Determination of the whole base sequence of the cDNA
10 insert of clone HP10246 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 110-bp 5'-untranslated region, a 675-bp ORF, and a 79-bp 3'-untranslated region. The ORF codes for a protein consisting of 224 amino acid residues and there
15 existed five putative transmembrane domains. Figure 45 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 23 kDa that was somewhat smaller than the
20 molecular weight of 25,244 predicted from the ORF. When expressed in COS7 cells, an expression product of about 21 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the
25 protein was similar to the human putative seven transmembrane domain protein (GenBank Accession No. Y18007). Table 31 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human putative seven transmembrane domain protein (TM).
30 Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that

of the protein of the present invention, respectively. The both proteins shared a homology of 93.3% in the entire region.

5

Table 31

```

HP MTLFHFNGCFALAYFPYFITYKCSGLSEYNAFWKCVQAGVTYLFVQLCKMLFLATFFPTW
*****.*****
TM MTLFHFNGCFALAYFPYFITYKCTDLSEYNAFWKCVQAGVTYLFVQLCKMLFLATFFPTW
10 HP EGGIYDFIGEFMKASVDVADLIGLNLVMSRNAGKGEYKIMVAALGWATAELIMSRCIPLW
*****
TM EGGIYDFIGEFMKASVDVADLIGLNLVMSRNAGKGEYKIMVAALGWATAELIMSRCIPLW
HP VGARGIEFDWKYIQMSIDSNISLVHYIVASAQVWMITRYDLYHTFRPAVLLLMFLSVYKA
*****.*****.****
15 TM VGARGIEFDWKYIQMSIDSNISLGPYIVASAQVWMITRYDLYHTFRPAVLLLMFLRVYKA
HP FVMETFVHLC SLG SWAALLARAVVTGLLALSTLALYVAVVNVHS
*****.*.*.***.....*.*****
TM FVMETFVHLC SLG SWAVLMAGVVVKGLLVIRNLAMYVAVVNVHS

```

20

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA453931) in ESTs, but, since they

25 are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

30

<HP10392> (SEQ ID Nos. 126, 136, and 146)

Determination of the whole base sequence of the cDNA insert of clone HP10392 obtained from cDNA library of human osteosarcoma cell line U-2 OS revealed the structure

consisting of a 24-bp 5'-untranslated region, a 777-bp ORF, and a 726-bp 3'-untranslated region. The ORF codes for a protein consisting of 258 amino acid residues and there existed a putative secretory signal at the N-terminus.

5 Figure 46 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 34 kDa that was somewhat larger than the molecular weight of 29,623 predicted from the ORF.
10 Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from leucine at position 49.

Furthermore, the search of the GenBank using the base
15 sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H15999) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein
20 of the present invention. In addition, partial identity with the hypothetical protein KIAA0384 (Accession No. AB002382) was observed, although the hypothetical protein had a different ORF.

25 <HP10489> (SEQ ID Nos. 127, 137, and 147)

Determination of the whole base sequence of the cDNA insert of clone HP10489 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 137-bp 5'-untranslated region, a 333-bp ORF, and a 189-bp 3'-
30 untranslated region. The ORF codes for a protein consisting of 110 amino acid residues and there existed two putative transmembrane domains. Figure 47 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 19 kDa that was somewhat larger than the molecular weight of 12,010 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA262162) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10519> (SEQ ID Nos. 128, 138, and 148)

Determination of the whole base sequence of the cDNA insert of clone HP10519 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 67-bp 5'-untranslated region, a 276-bp ORF, and a 367-bp 3'-untranslated region. The ORF codes for a protein consisting of 91 amino acid residues and there existed one putative transmembrane domain. Figure 48 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa that was almost identical with the molecular weight of 10,275 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W16639) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein

of the present invention.

<HP10531> (SEQ ID Nos. 129, 139, and 149)

Determination of the whole base sequence of the cDNA
5 insert of clone HP10531 obtained from cDNA library of human
osteosarcoma cell line Saos-2 revealed the structure
consisting of a 55-bp 5'-untranslated region, a 1035-bp ORF,
and a 1092-bp 3'-untranslated region. The ORF codes for a
protein consisting of 344 amino acid residues and there
10 existed five putative transmembrane domains. Figure 49
depicts the hydrophobicity/hydrophilicity profile, obtained
by the Kyte-Doolittle method, of the present protein. In
vitro translation resulted in formation of a translation
product of high molecular weight.

15 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. R50695) in ESTs, but, since they are
partial sequences, it can not be judged whether or not any
20 of these sequences codes for the same protein as the protein
of the present invention.

<HP10574> (SEQ ID Nos. 130, 140, and 150)

Determination of the whole base sequence of the cDNA
25 insert of clone HP10574 obtained from cDNA library of human
stomach cancer revealed the structure consisting of a 210-bp
5'-untranslated region, a 1287-bp ORF, and a 1276-bp 3'-
untranslated region. The ORF codes for a protein consisting
of 428 amino acid residues and there existed a putative
30 secretory signal at the N-terminus and one putative
transmembrane domain in the intermediate region. Figure 50
depicts the hydrophobicity/hydrophilicity profile, obtained

by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from serine at position 36.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Drosophila melanogaster GOLIATH protein (SWISS-PROT Accession No. Q06003). Table 32 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the D. melanogaster GOLIATH protein (DM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The intermediate region of 169 amino acids of the protein of the present invention shared a homology of 41.4% with the N-terminal region of the D. melanogaster GOLIATH protein.

Table 32

[illegible]

25 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. AA155685) in ESTs, but, since they
are partial sequences, it can not be judged whether or not
30 any of these sequences codes for the same protein as the
protein of the present invention.

INDUSTRIAL APPLICABILITY

The present invention provides human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as well as eucaryotic cells expressing these DNAs. All of the proteins of the present invention are secreted or exist in the cell membrane, so that they are considered to be proteins controlling the proliferation and/or the differentiation of the cells. Accordingly, the proteins of the present invention can be employed as pharmaceuticals such as carcinostatic agents which act to control the proliferation and/or the differentiation of the cells, or as antigens for preparing antibodies against these proteins. The DNAs of the present invention can be utilized as probes for the genetic diagnosis and gene sources for the gene therapy. Furthermore, the DNAs can be utilized for large-scale expression of these proteins. Cells into which these genes are introduced to express these proteins, can be utilized for detection of the corresponding receptors and ligands, screening of novel low-molecular pharmaceuticals, and so on.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or

primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, Trends Pharmacol. Sci. 15(7): 250-254; Lavarosky et al., 1997, Biochem. Mol. Med. 62(1): 11-22; and Hampel, 1998, Prog. Nucleic Acid Res. Mol. Biol. 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished

through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, Bioessays 14(9): 629-633; Zwaal et al., 1993, Proc. Natl. Acad. Sci. USA 90(16): 7431-7435; Clark et al., 1994, Proc. Natl. Acad. Sci. USA 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour et al., 1988, Nature 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614, 396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s). Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more

preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide, as determined by those of skill in the art. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous, or related to that encoded by the polynucleotides.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides

capable of hybridizing under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the

5 table 33 below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 33

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [‡]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
A	DNA : DNA	≥50	65°C; 1×SSC -or- 42°C; 1×SSC, 50% formamide	65°C; 0.3×SSC
B	DNA : DNA	<50	T _B [*] ; 1×SSC	T _B [*] ; 1×SSC
C	DNA : RNA	≥50	67°C; 1×SSC -or- 45°C; 1×SSC, 50% formamide	67°C; 0.3×SSC
D	DNA : RNA	<50	T _D [*] ; 1×SSC	T _D [*] ; 1×SSC
E	RNA : RNA	≥50	70°C; 1×SSC -or- 50°C; 1×SSC, 50% formamide	70°C; 0.3×SSC
F	RNA : RNA	<50	T _F [*] ; 1×SSC	T _F [*] ; 1×SSC
G	DNA : DNA	≥50	65°C; 4×SSC -or- 42°C; 4×SSC, 50% formamide	65°C; 1×SSC
H	DNA : DNA	<50	T _H [*] ; 4×SSC	T _H [*] ; 4×SSC
I	DNA : RNA	≥50	67°C; 4×SSC -or- 45°C; 4×SSC, 50% formamide	67°C; 1×SSC
J	DNA : RNA	<50	T _J [*] ; 4×SSC	T _J [*] ; 4×SSC
K	RNA : RNA	≥50	70°C; 4×SSC -or- 50°C; 4×SSC, 50% formamide	67°C; 1×SSC
L	RNA : RNA	<50	T _L [*] ; 2×SSC	T _L [*] ; 2×SSC
M	DNA : DNA	≥50	50°C; 4×SSC -or- 40°C; 6×SSC, 50% formamide	50°C; 2×SSC
N	DNA : DNA	<50	T _N [*] ; 6×SSC	T _N [*] ; 6×SSC
O	DNA : RNA	≥50	55°C; 4×SSC -or- 42°C; 6×SSC, 50% formamide	55°C; 2×SSC
P	DNA : RNA	<50	T _P [*] ; 6×SSC	T _P [*] ; 6×SSC
Q	RNA : RNA	≥50	60°C; 4×SSC -or- 45°C; 6×SSC, 50% formamide	60°C; 2×SSC
R	RNA : RNA	<50	T _R [*] ; 4×SSC	T _R [*] ; 4×SSC

‡ : The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

† : SSPE (1×SSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH7.4) can be substituted for SSC (1×SSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R : The hybridization temperature for hybrids anticipated to be less than

50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, $T_m(^{\circ}\text{C}) = 2(\text{\# of A + T bases}) + 4(\text{\# of G + C bases})$. For hybrids between 18 and 49 base pairs in length, $T_m(^{\circ}\text{C}) = 81.5 + 16.6(\log_{10}[\text{Na}^+]) + 0.41(\% \text{G+C}) - (600/N)$, where N is the number of bases in the hybrid, and $[\text{Na}^+]$ is the concentration of sodium ions in the hybridization buffer ($[\text{Na}^+]$ for $1\times\text{SSC}=0.165\text{M}$).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and Current Protocols in Molecular Biology, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

CLAIMS

1. A protein comprising any one of an amino acid
sequence selected from the group consisting of SEQ ID Nos. 1
5 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130.

2. An isolated DNA coding for the protein according
to Claim 1.

3. An isolated cDNA comprising any one of a base
sequence selected from the group consisting of SEQ ID Nos.
10 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140.

4. The cDNA according to Claim 3 consisting of any
one of a base sequence selected from the group consisting of
SEQ ID Nos. 21 to 30, 51 to 60, 81 to 90, 111 to 120, and
141 to 150.

15 5. An expression vector that is capable of expressing
the DNA according to any one of Claim 2 to Claim 4 by in
vitro translation or in eucaryotic cells.

6. A transformed eucaryotic cell that is capable of
expressing the DNA according to any one of Claim 2 to Claim
20 4 and of producing the protein according to Claim 1.

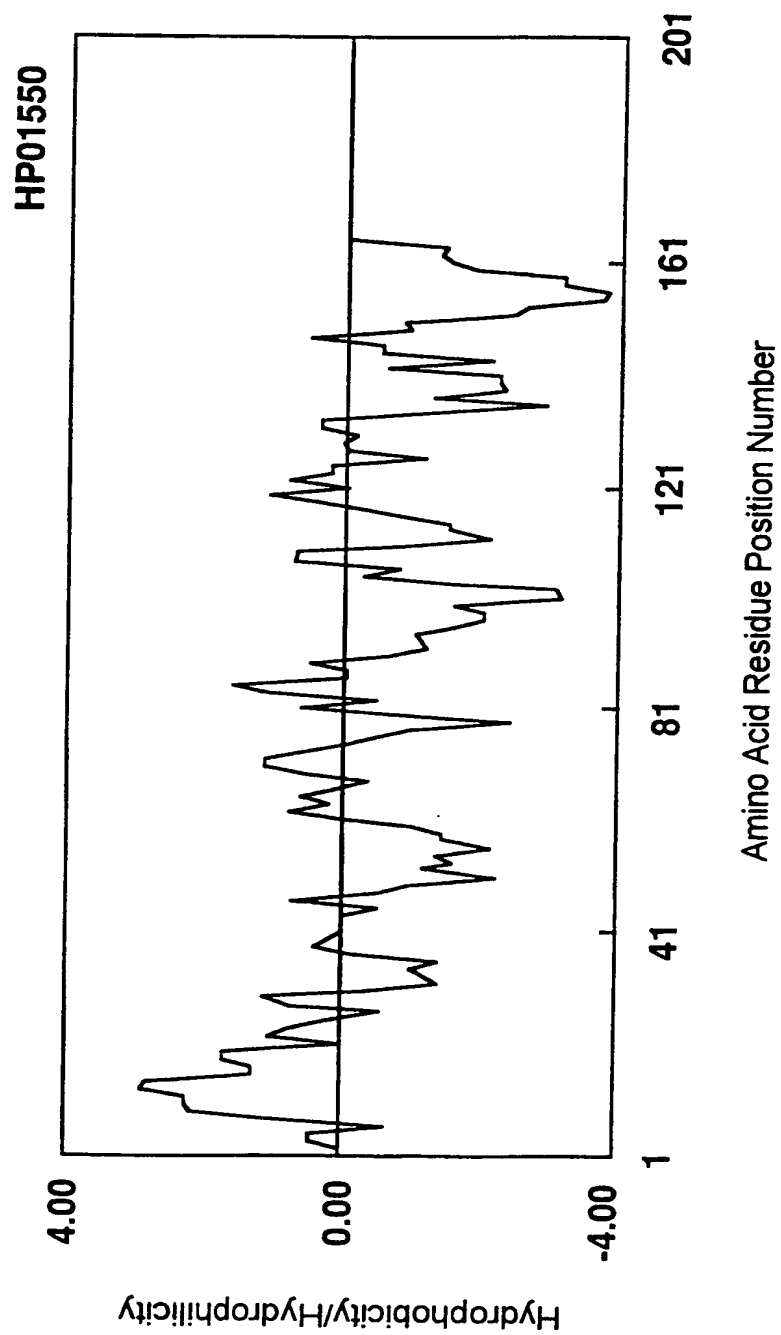


Fig. 1

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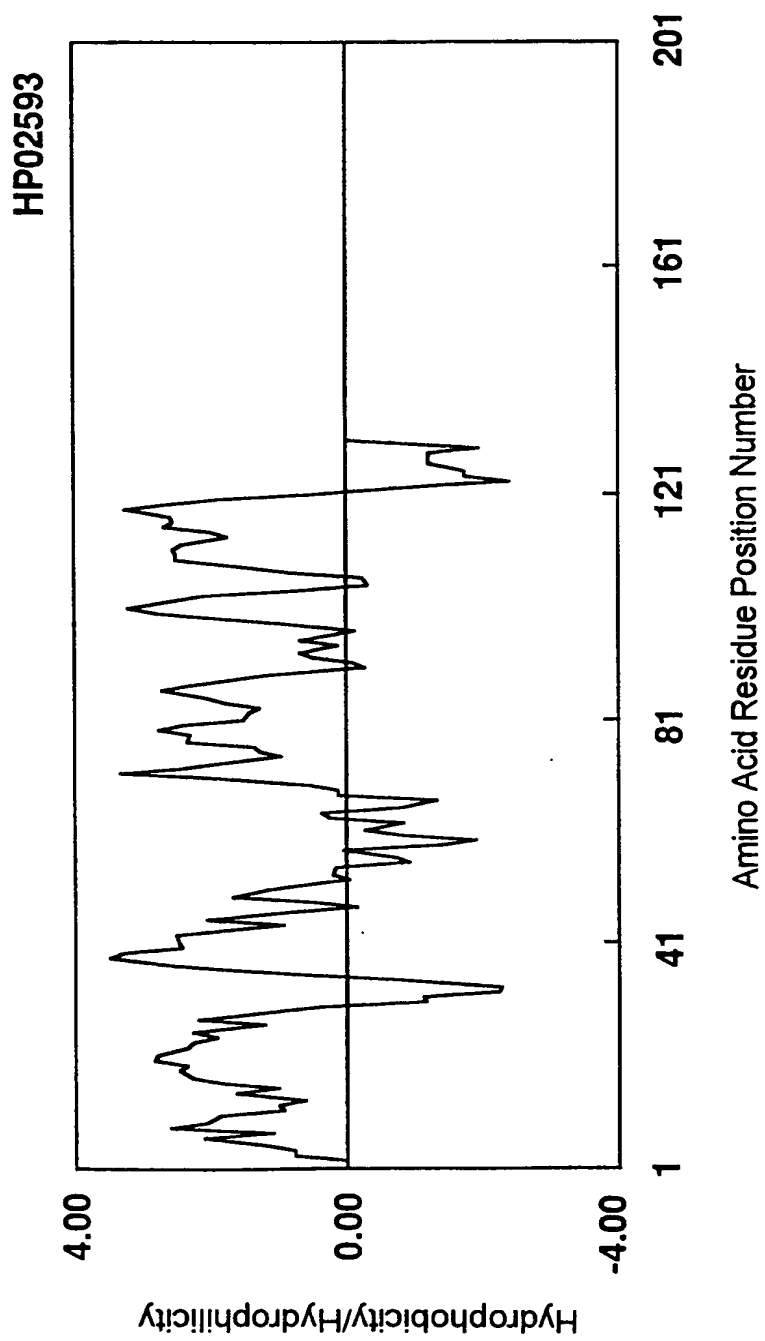


Fig. 2

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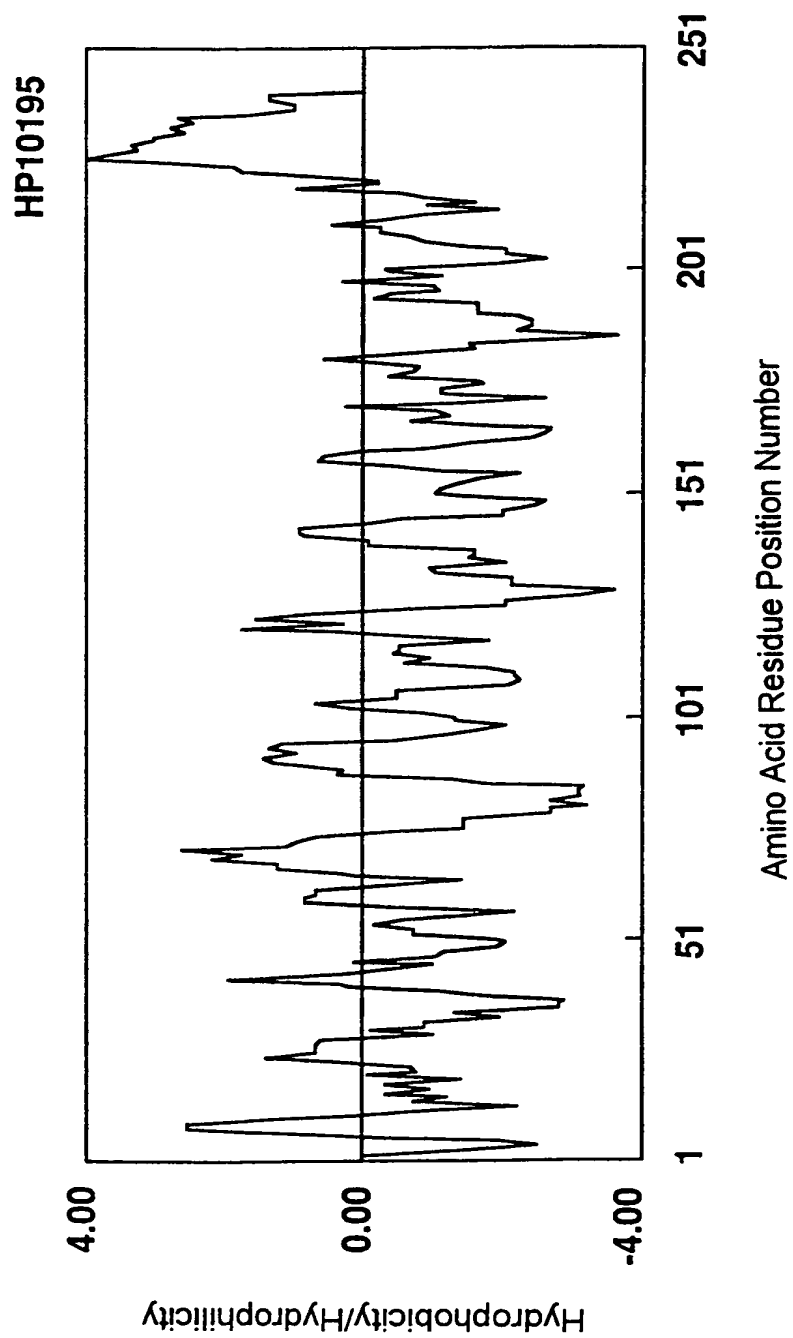


Fig. 3

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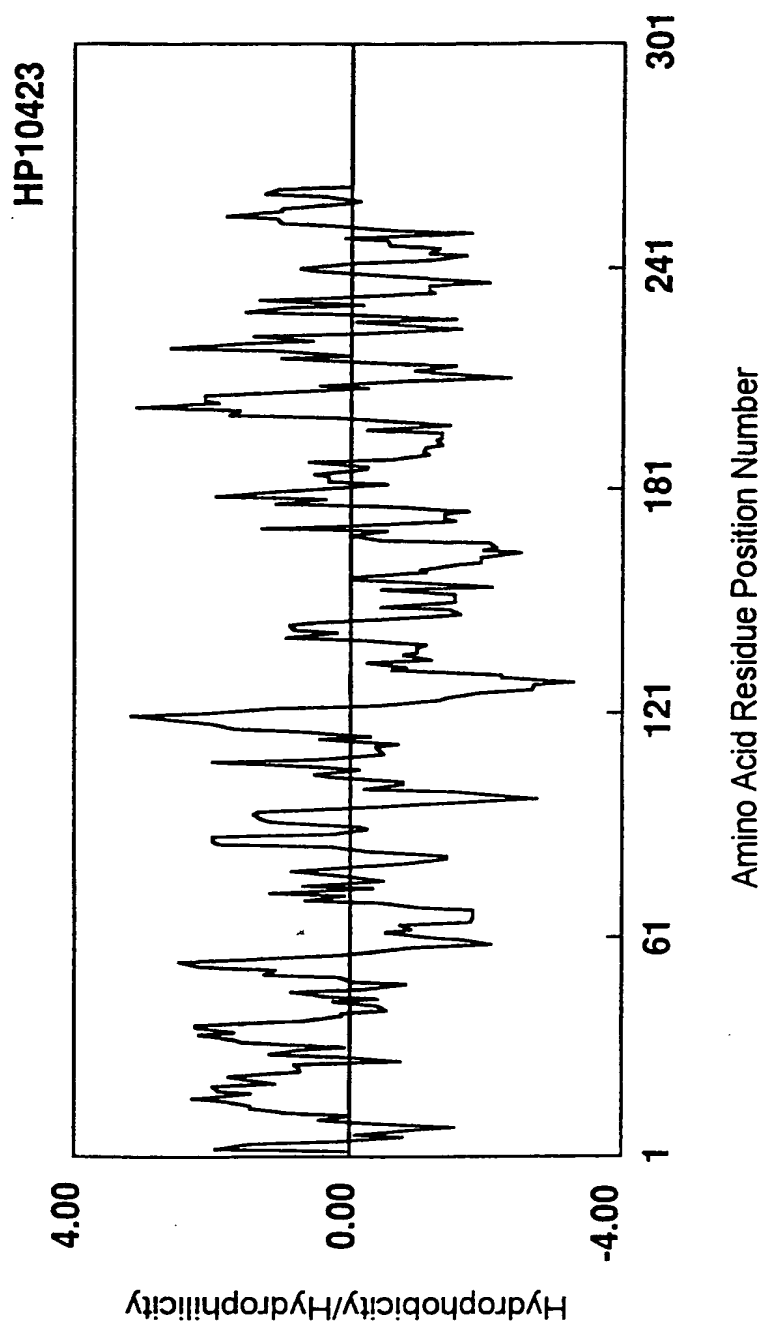


Fig. 4

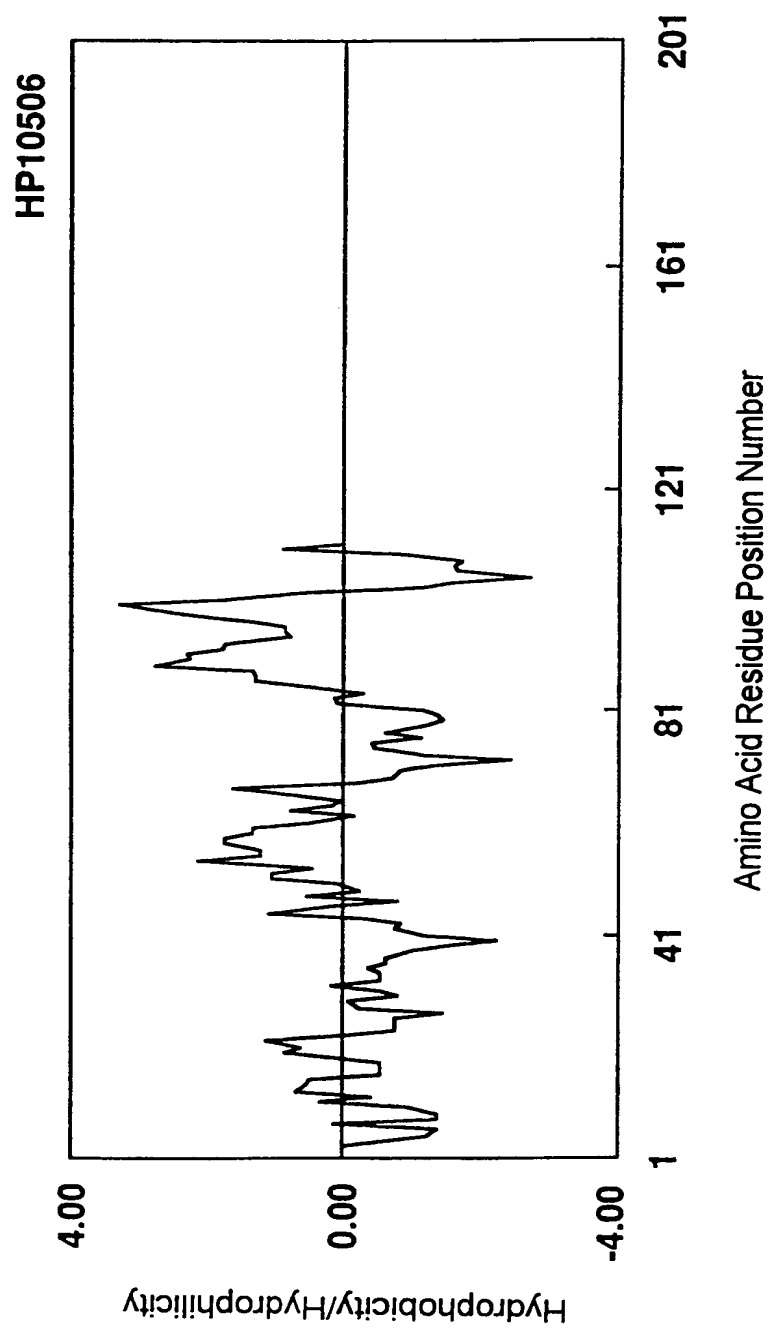


Fig. 5

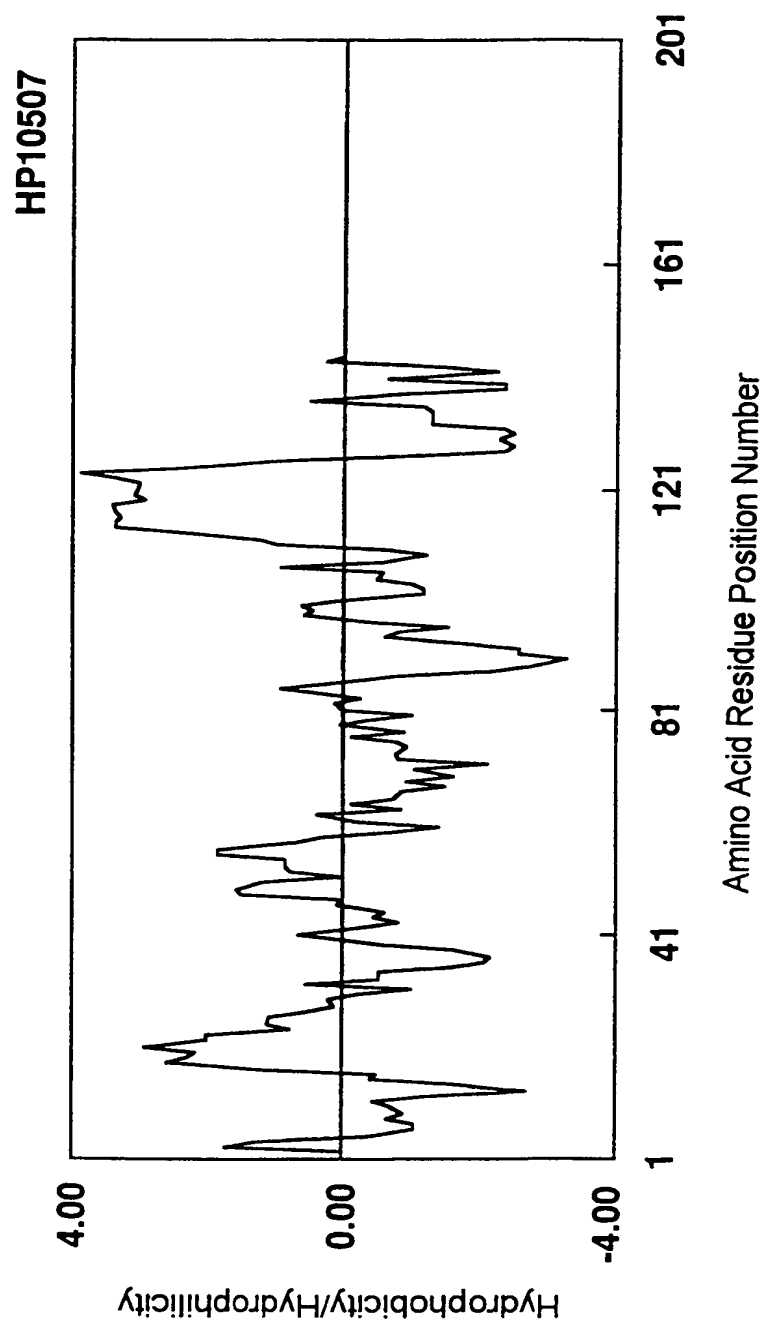


Fig. 6

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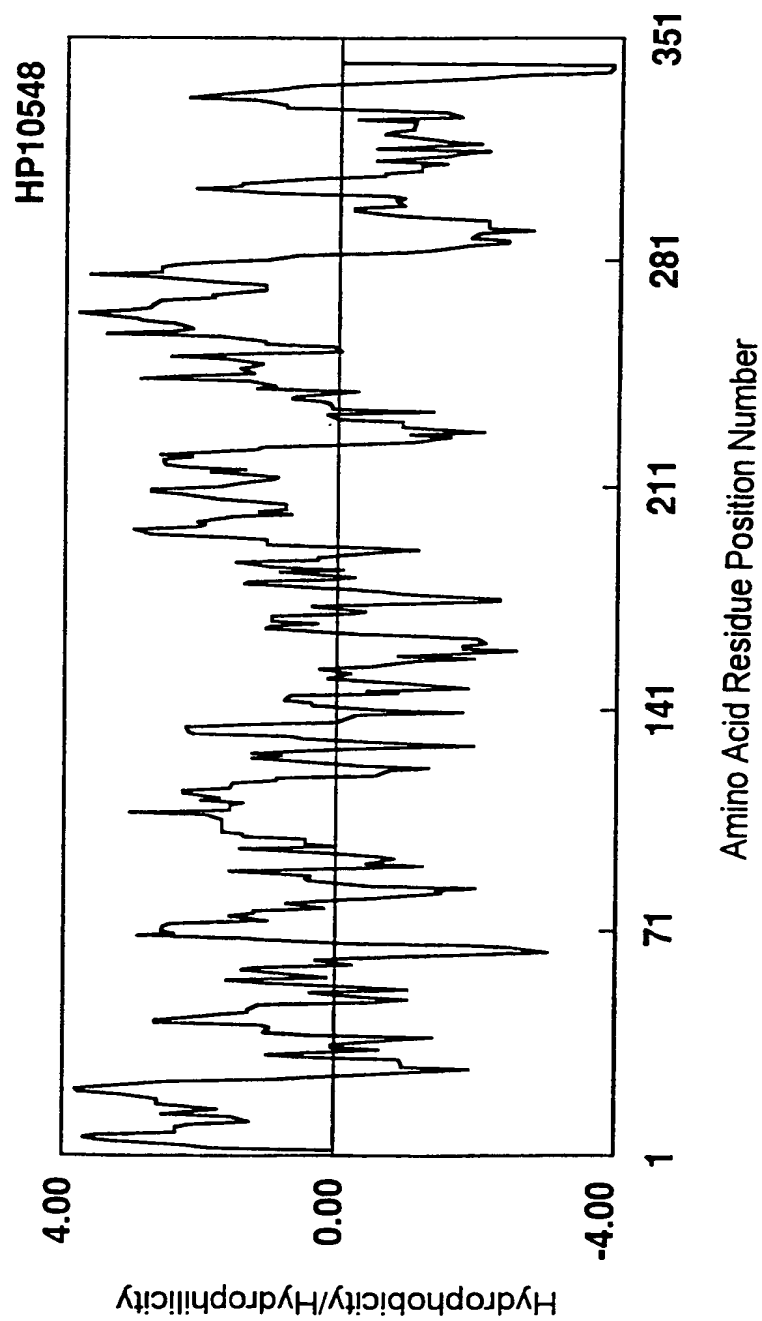


Fig. 7

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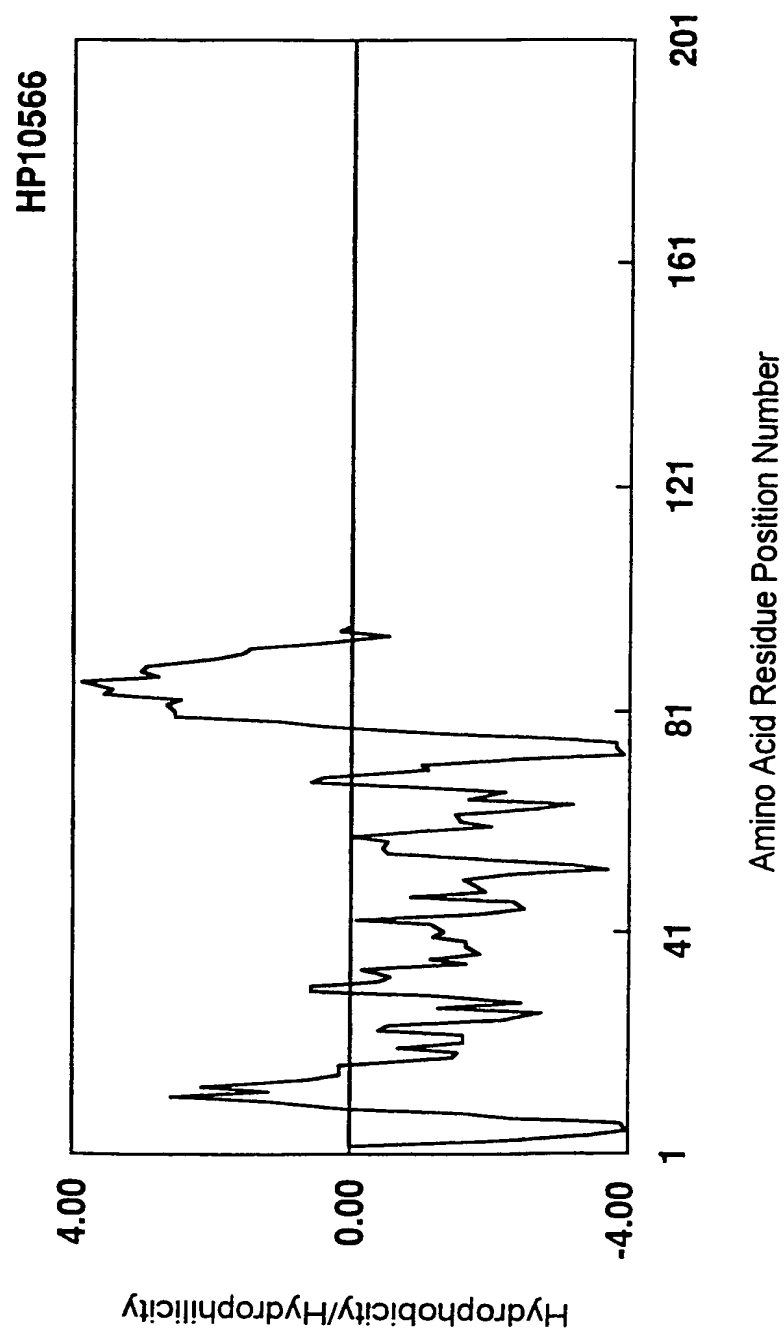


Fig. 8

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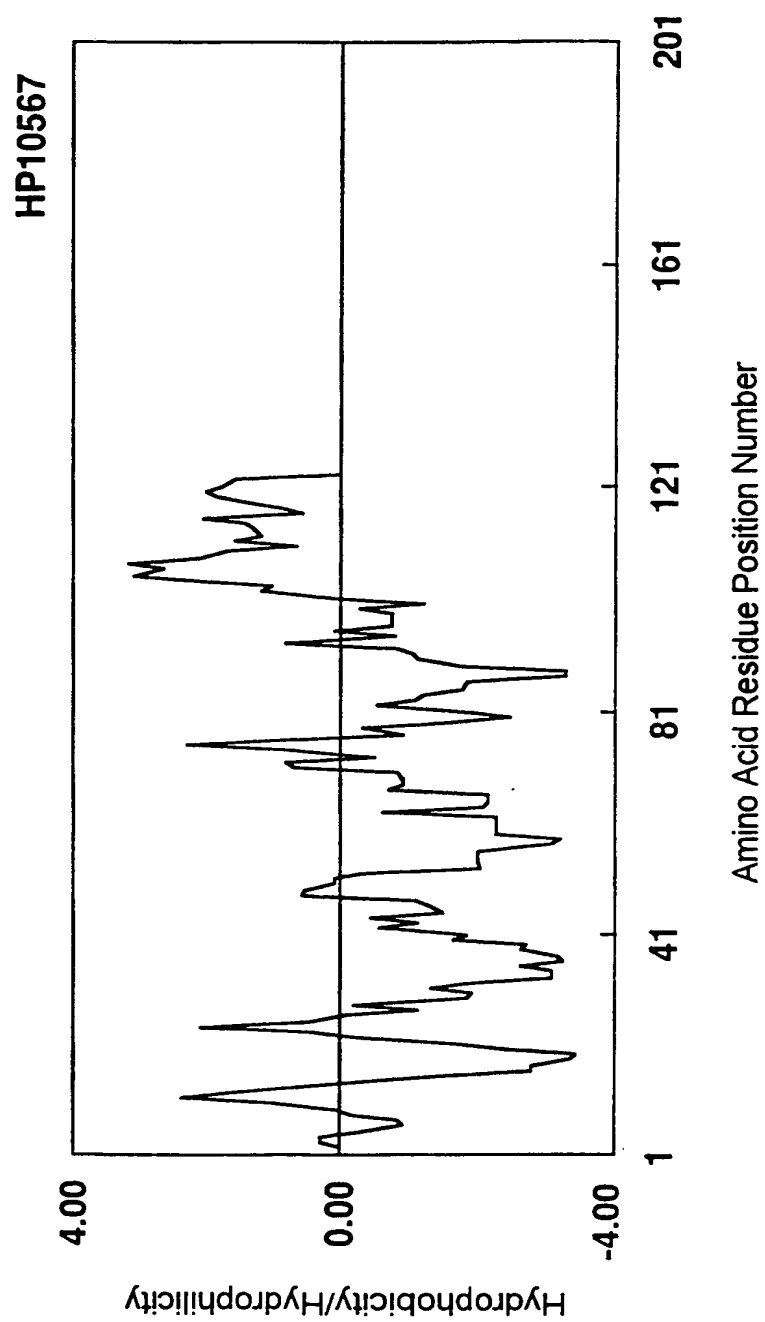


Fig. 9

10/50

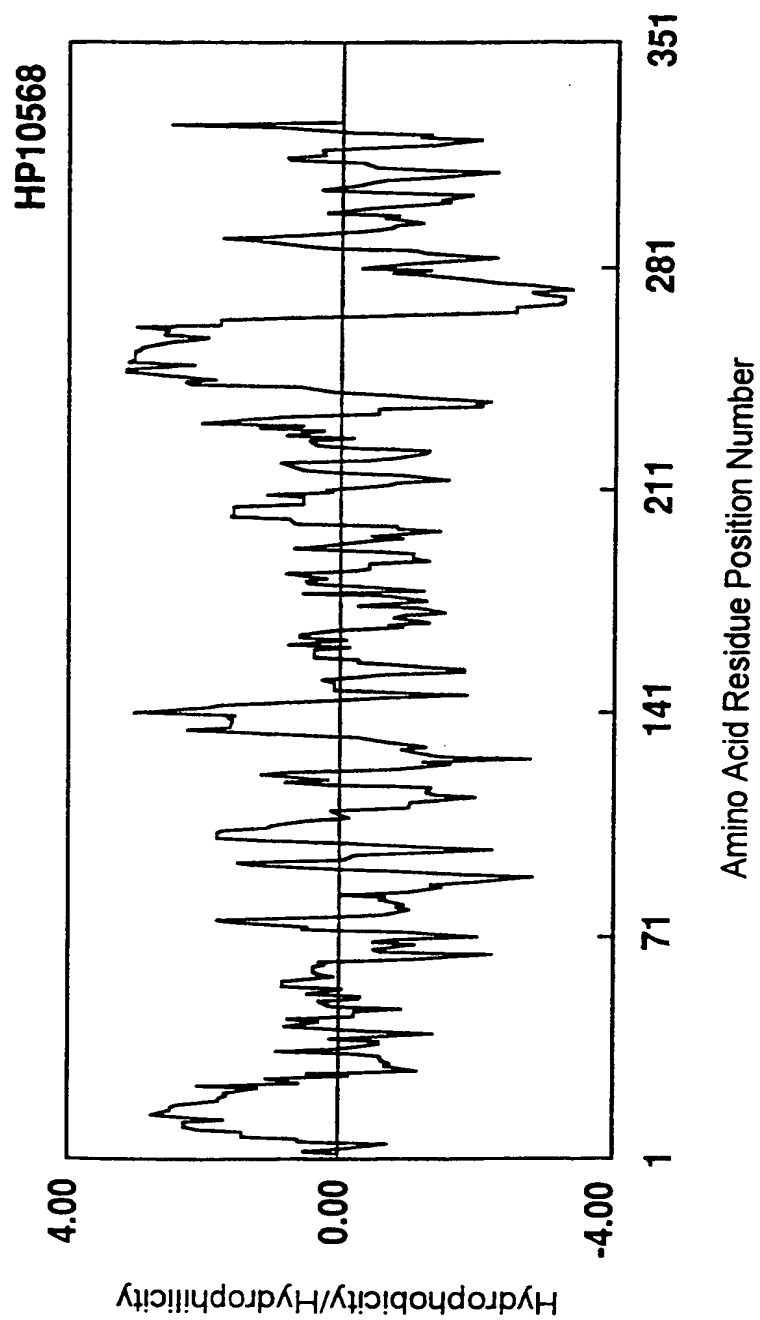


Fig. 10

11/50

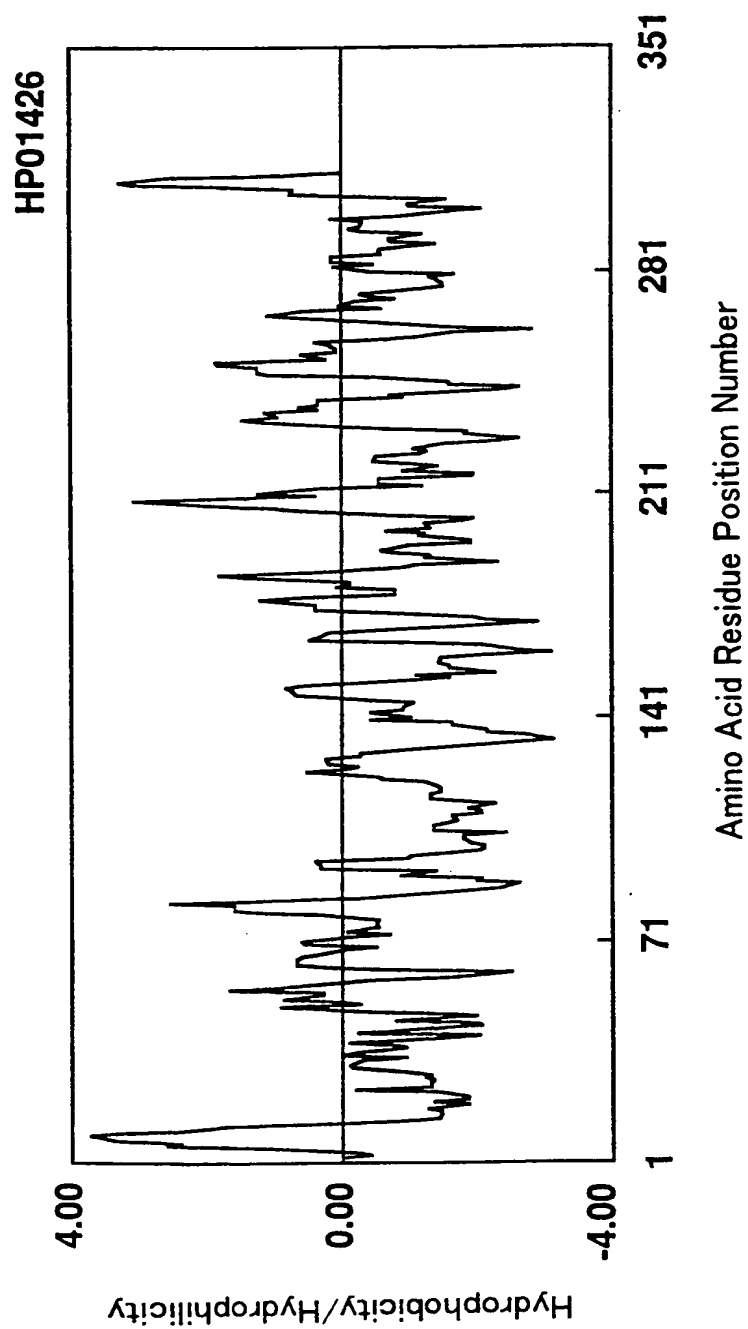


Fig. 11

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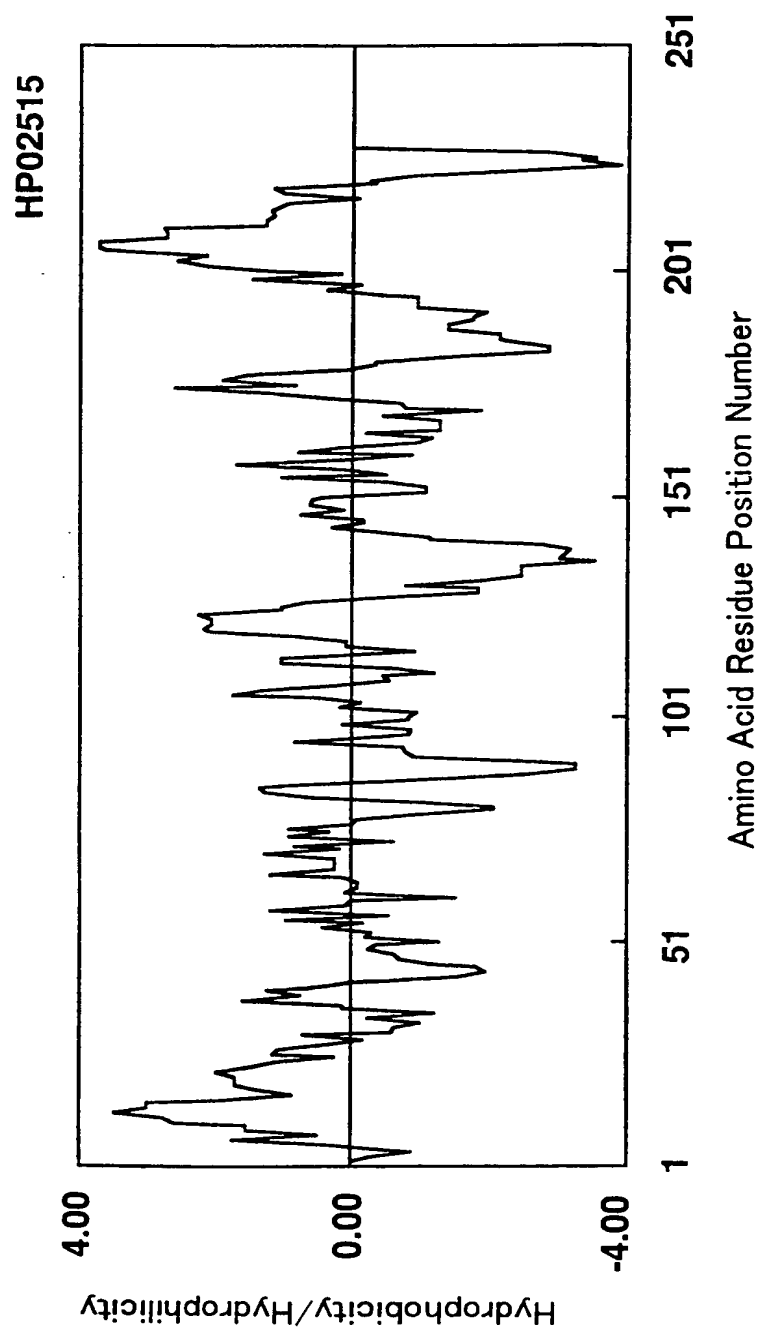


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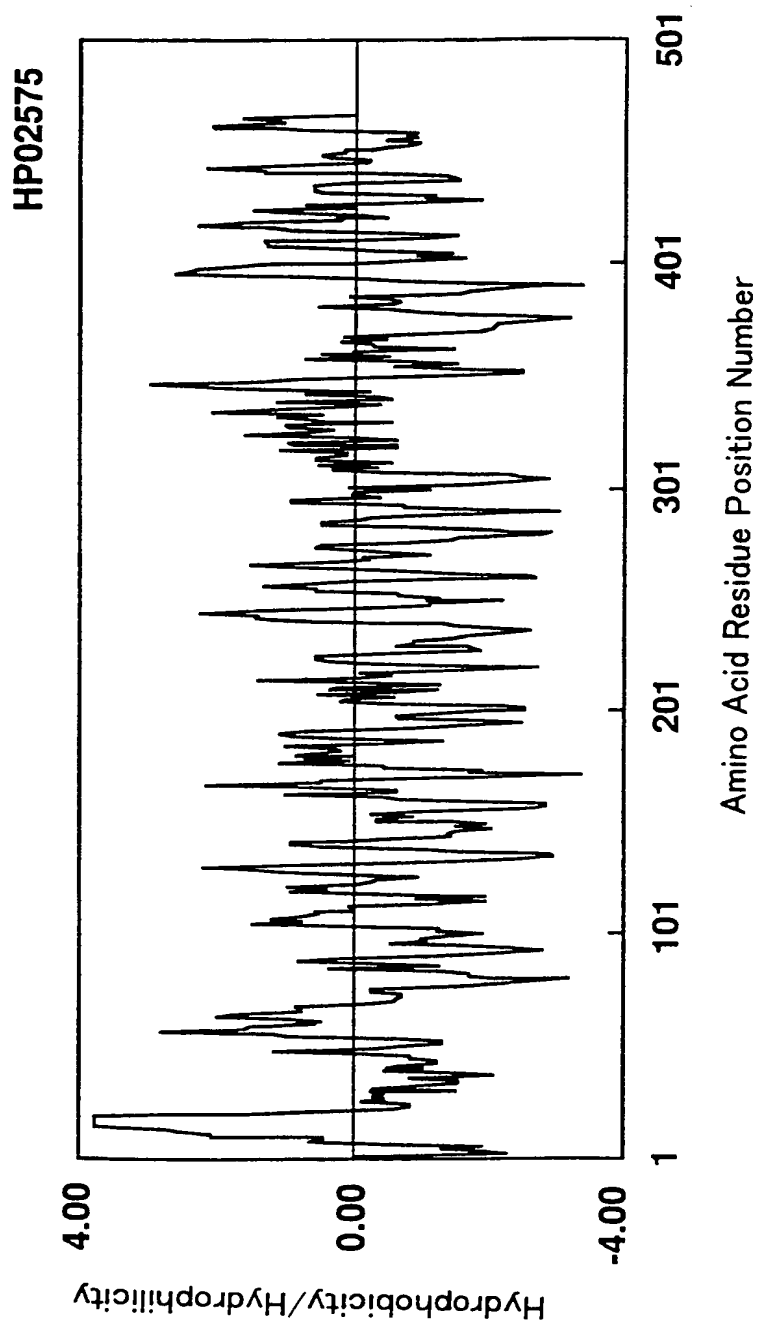


Fig. 13

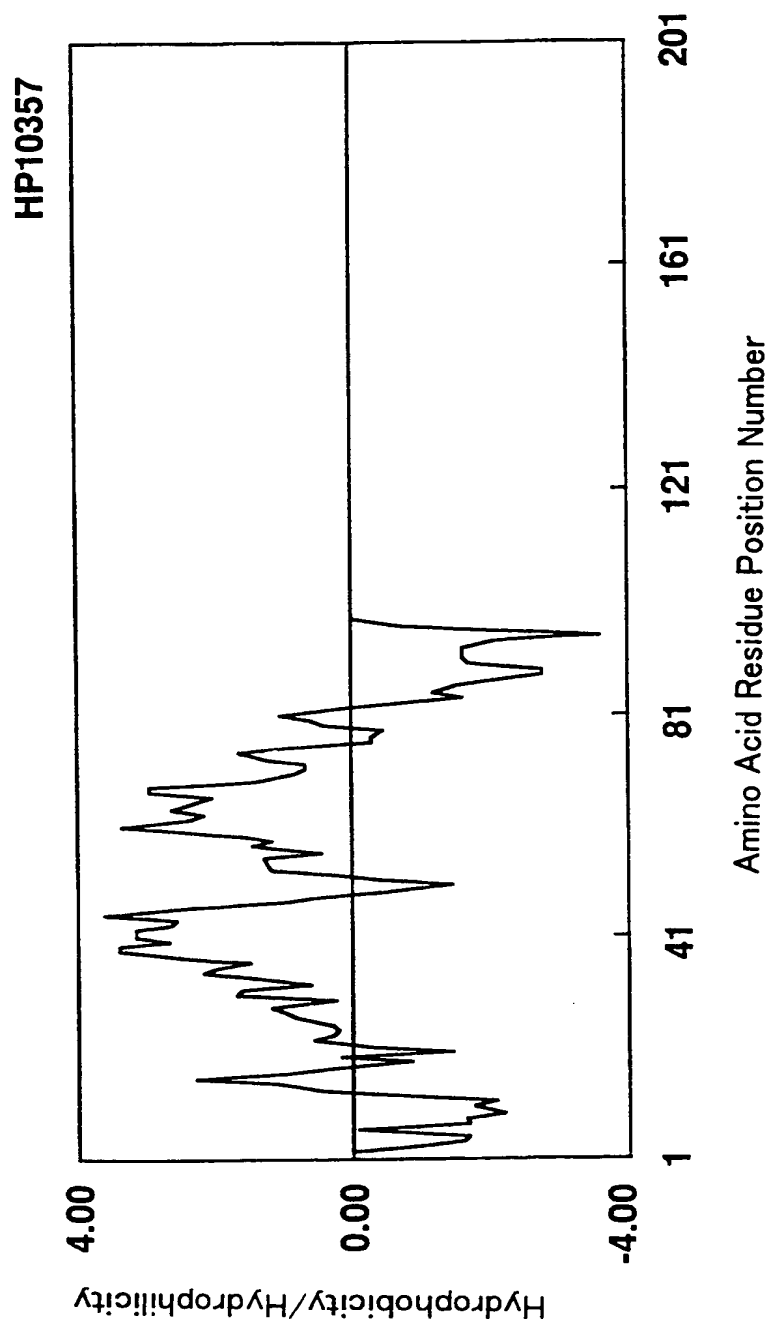


Fig. 14

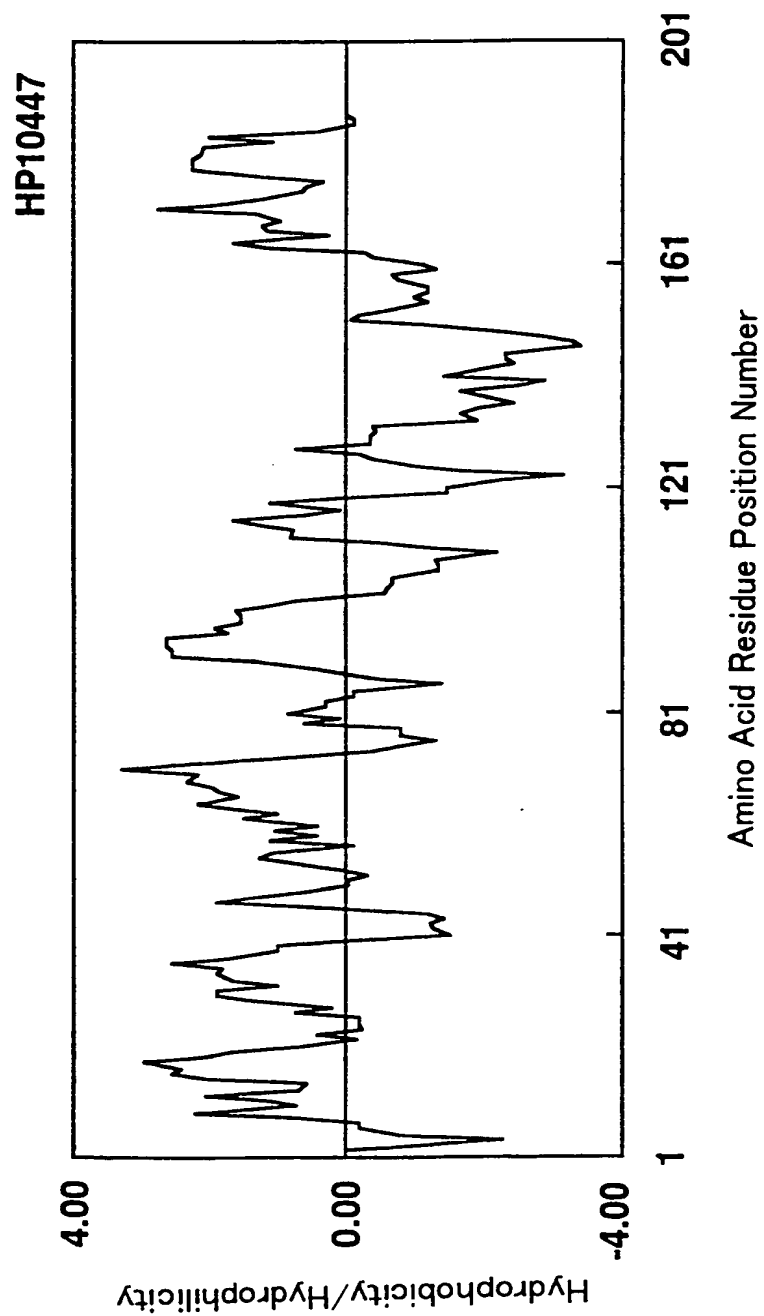


Fig. 15

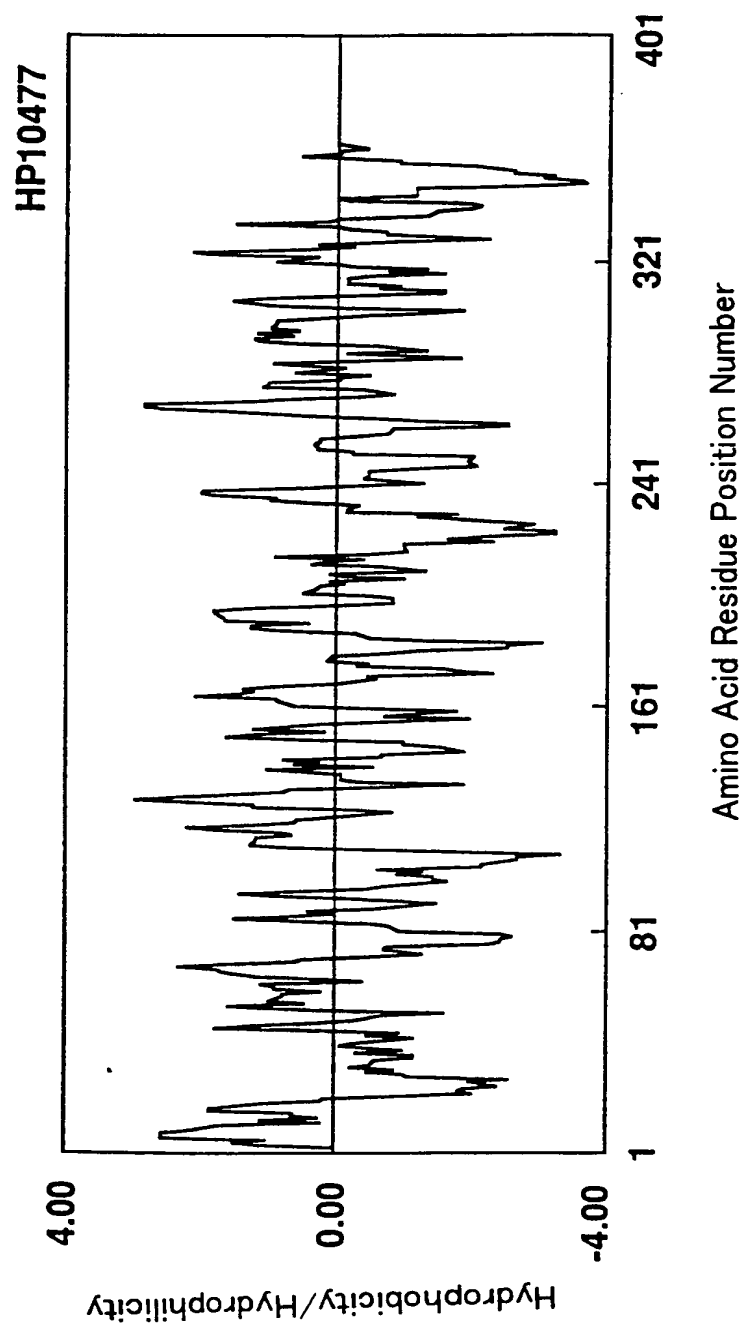


Fig. 16

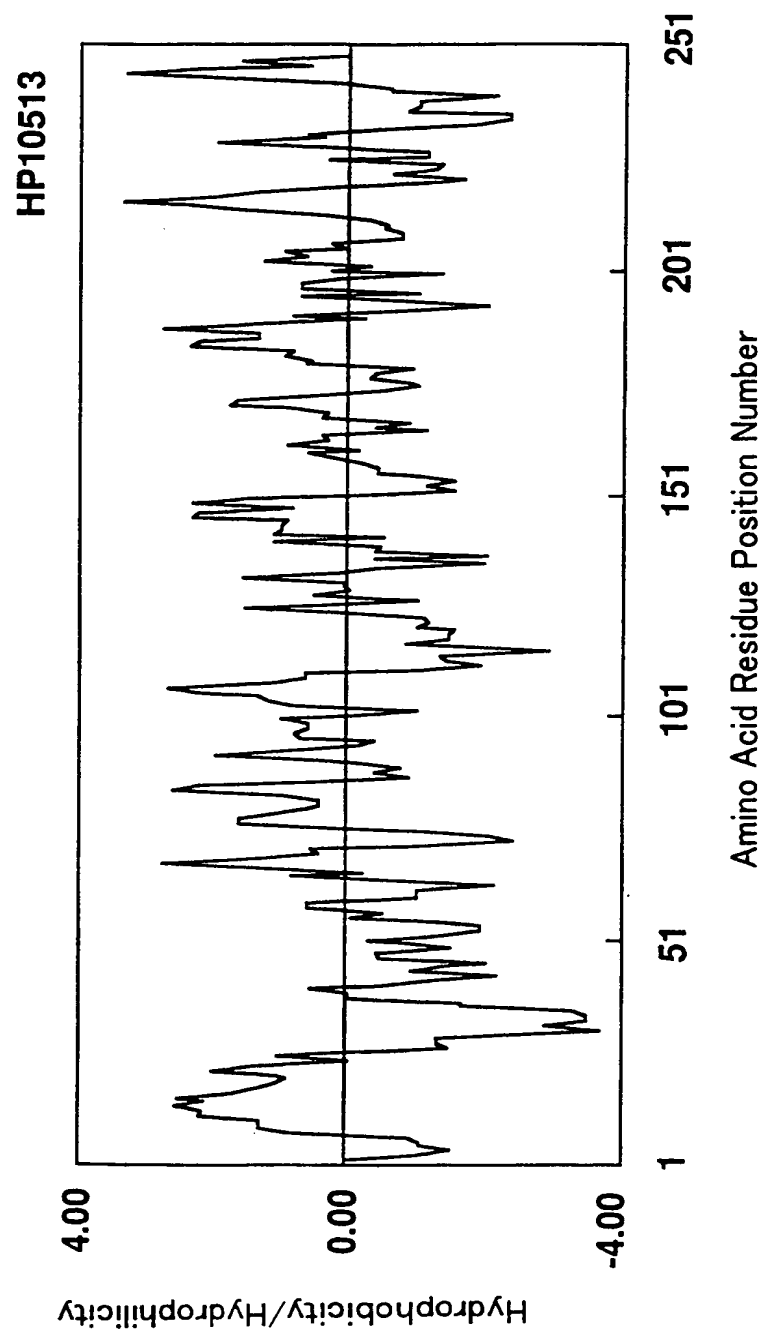


Fig.17

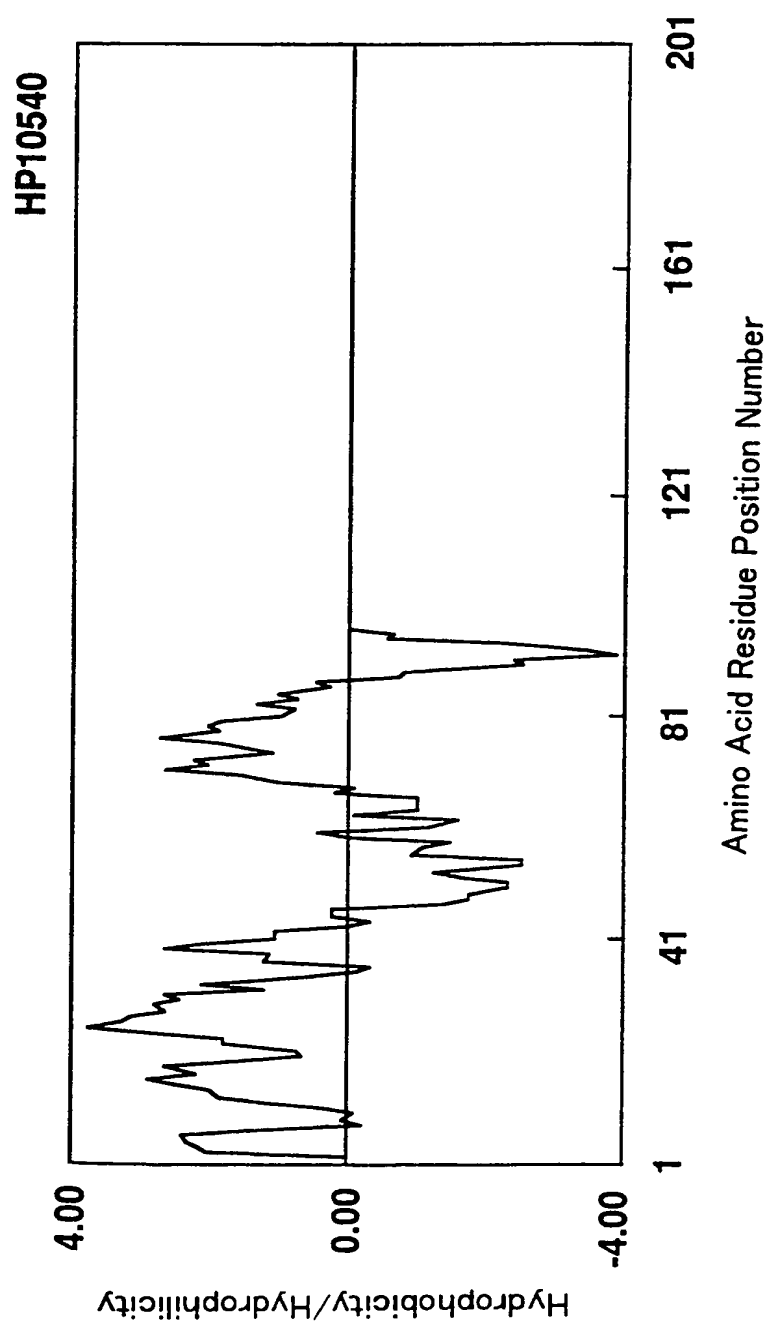


Fig. 18

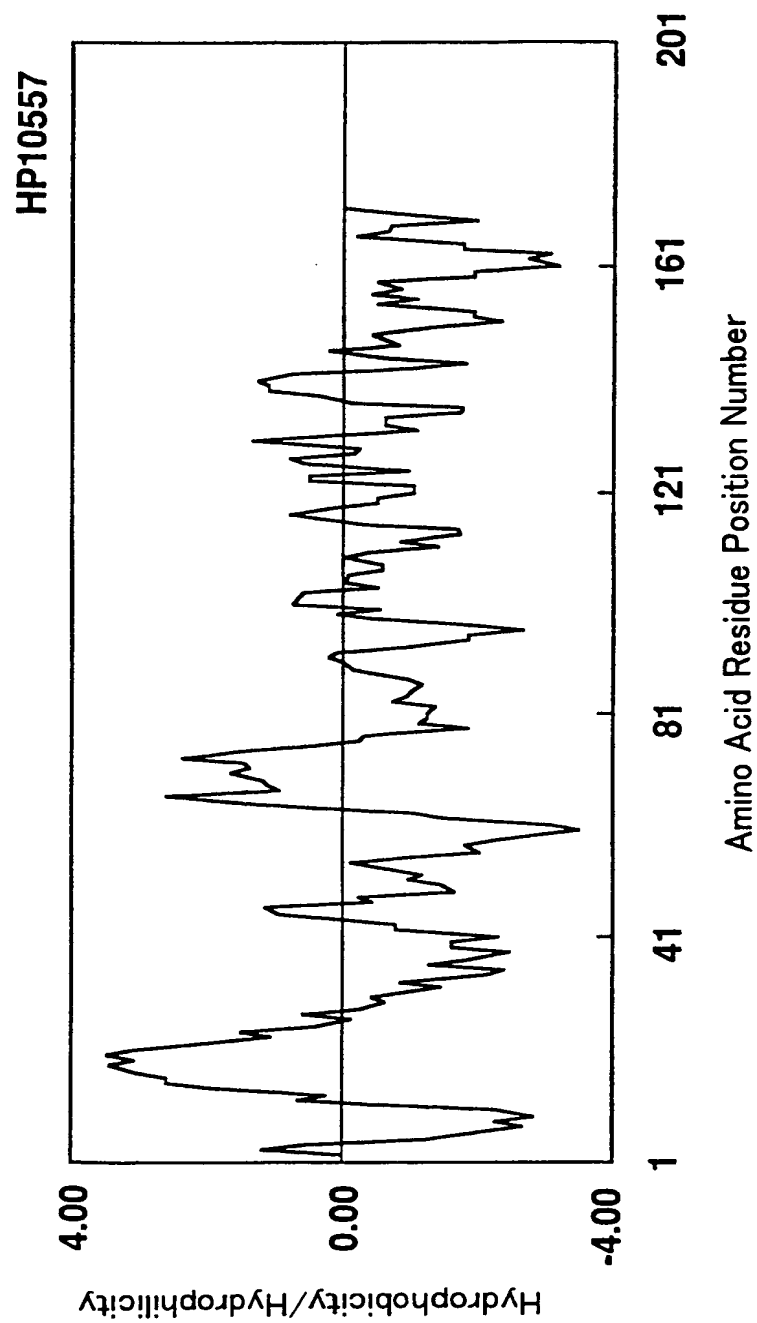


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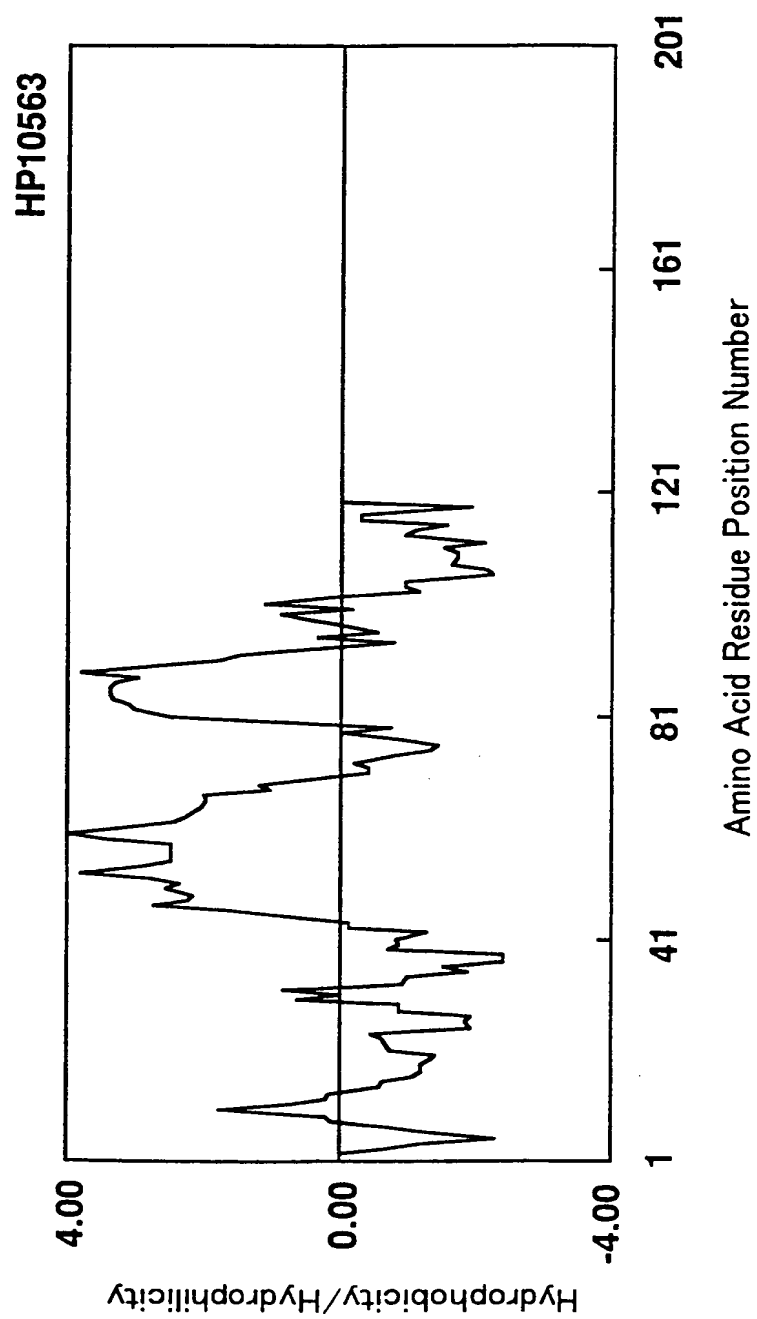


Fig. 20

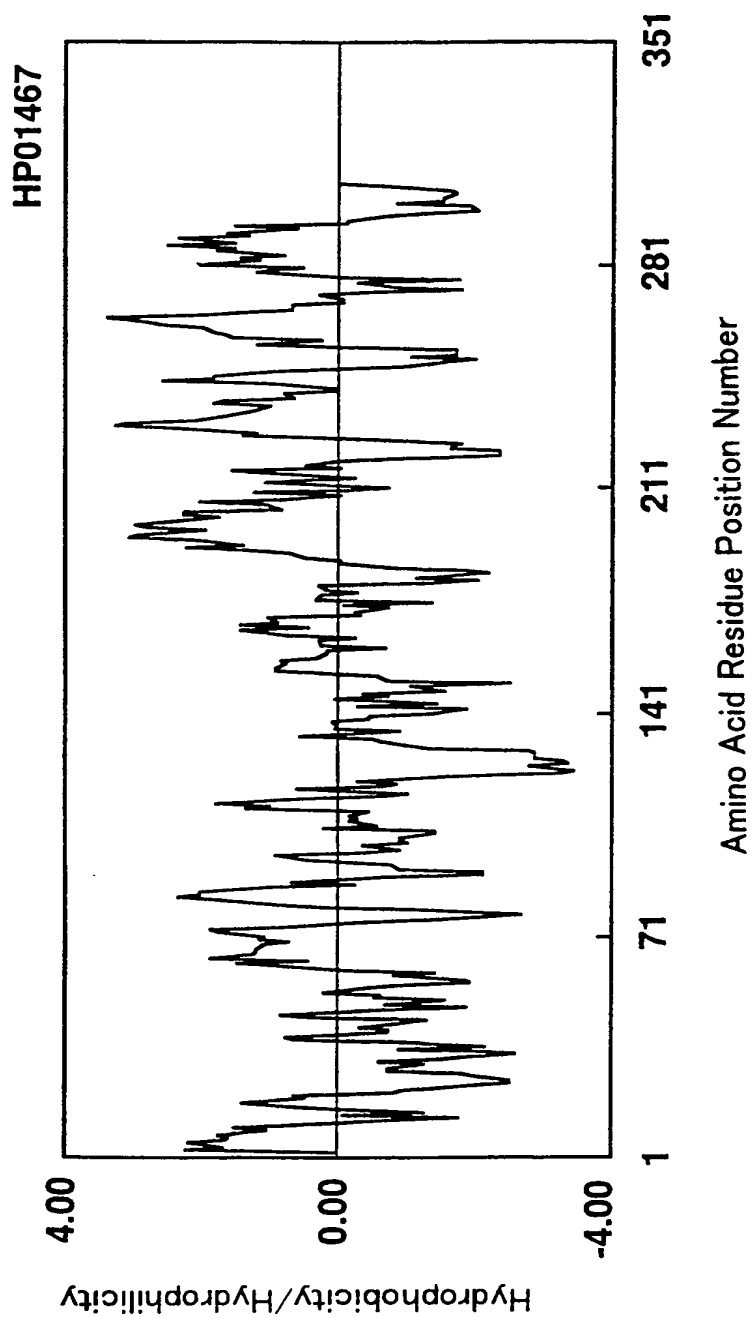


Fig. 21

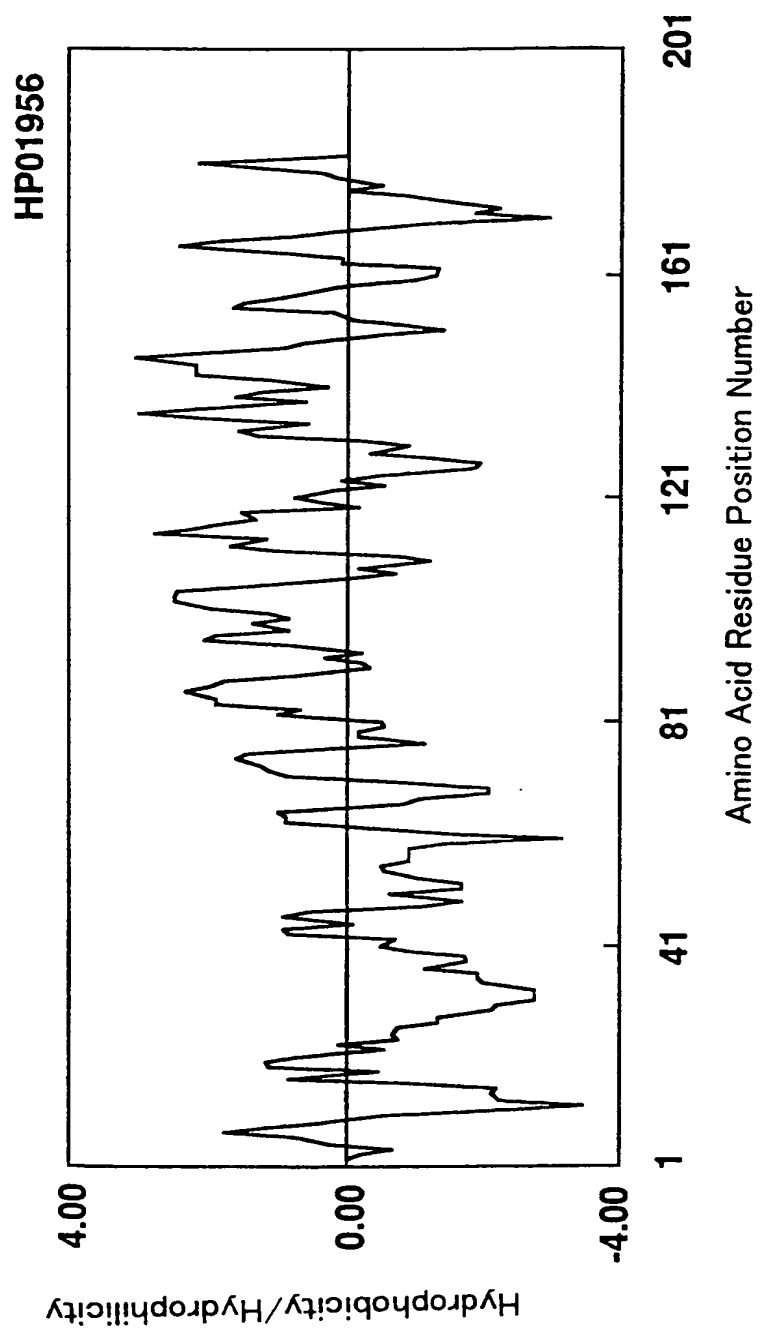


Fig.22

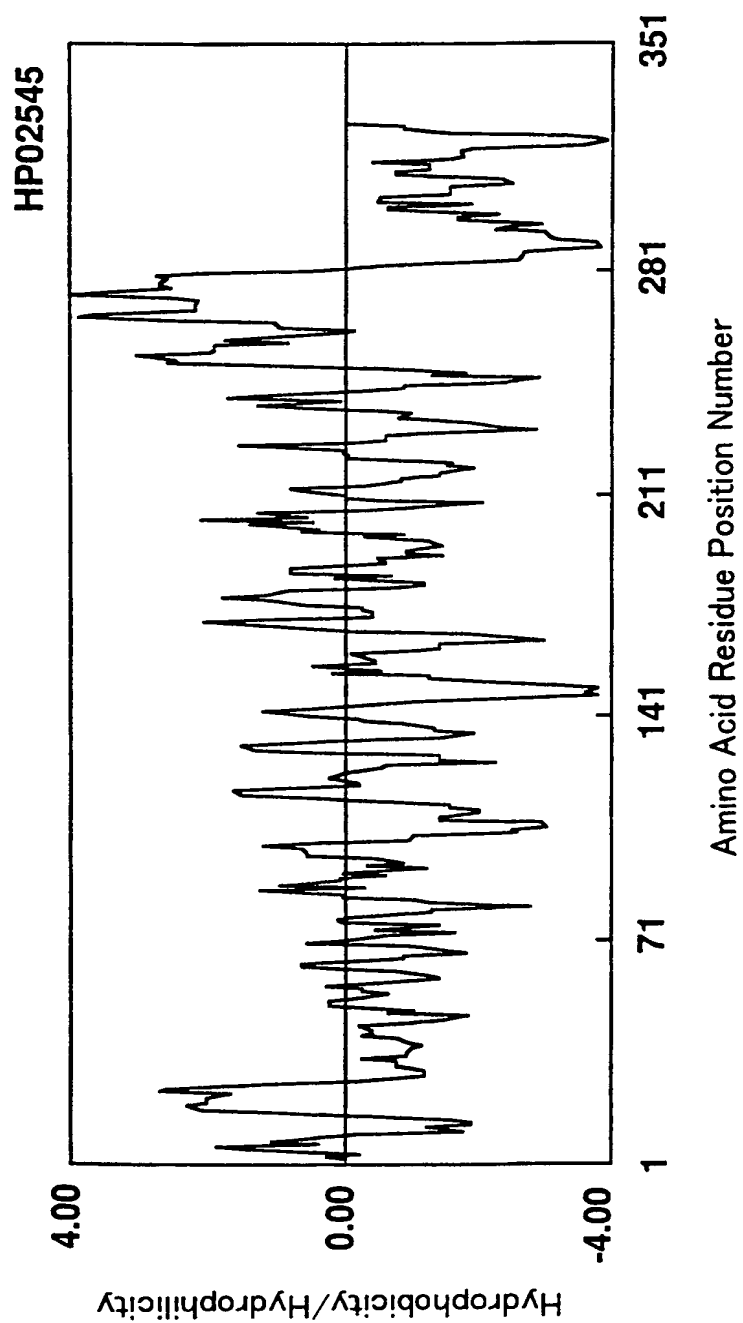


Fig. 23

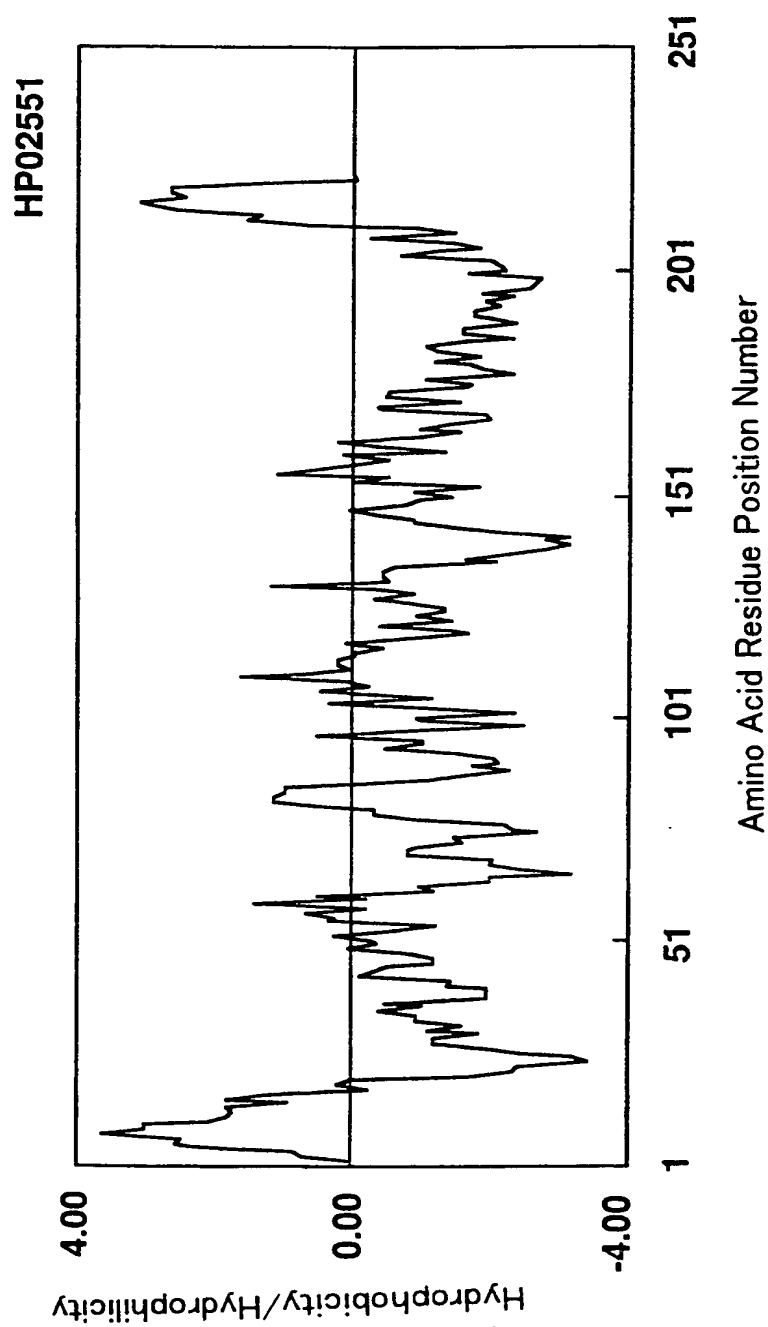


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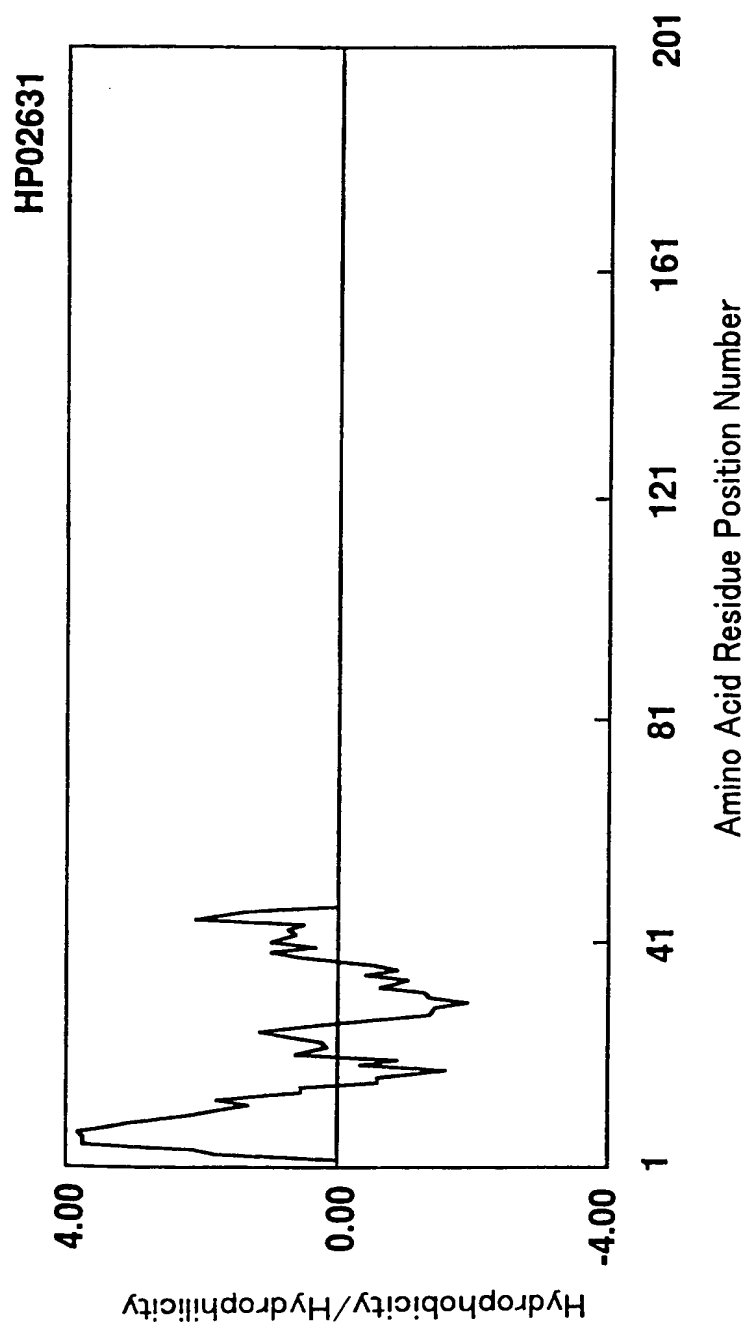


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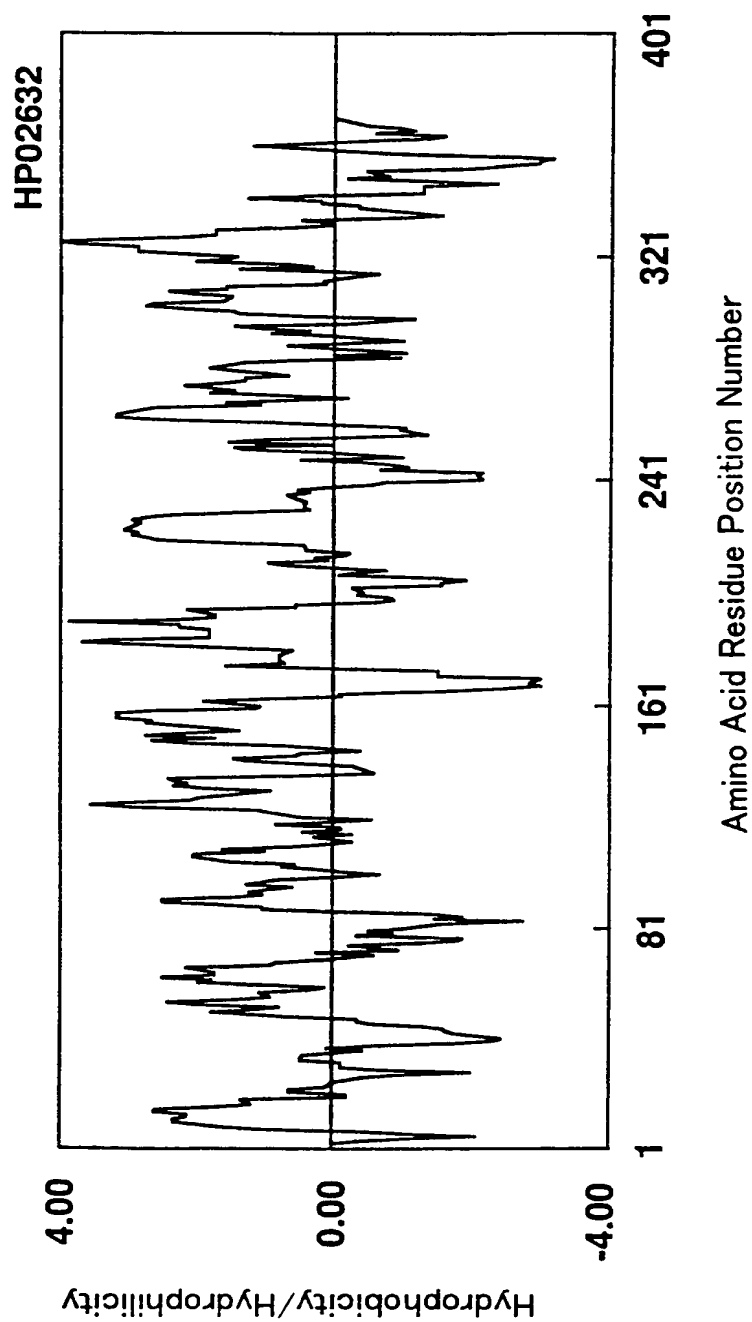


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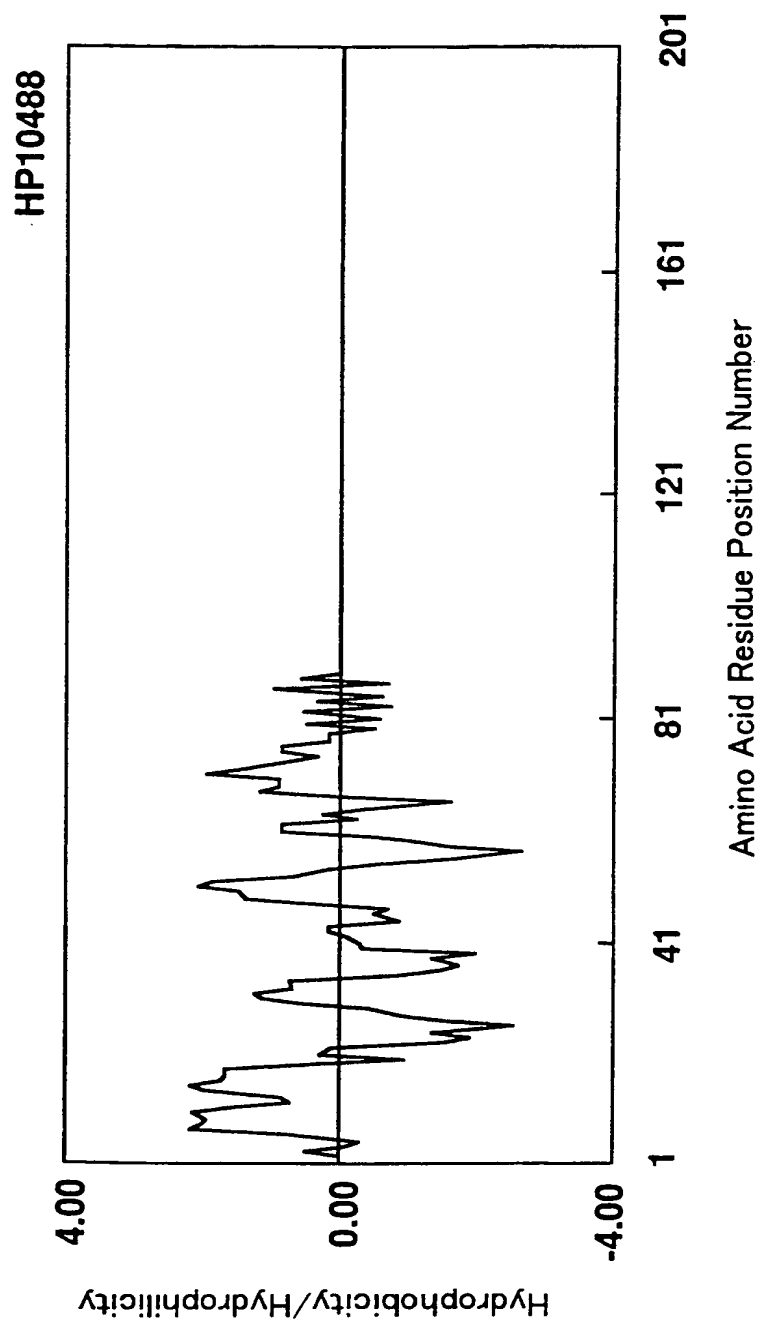


Fig.27

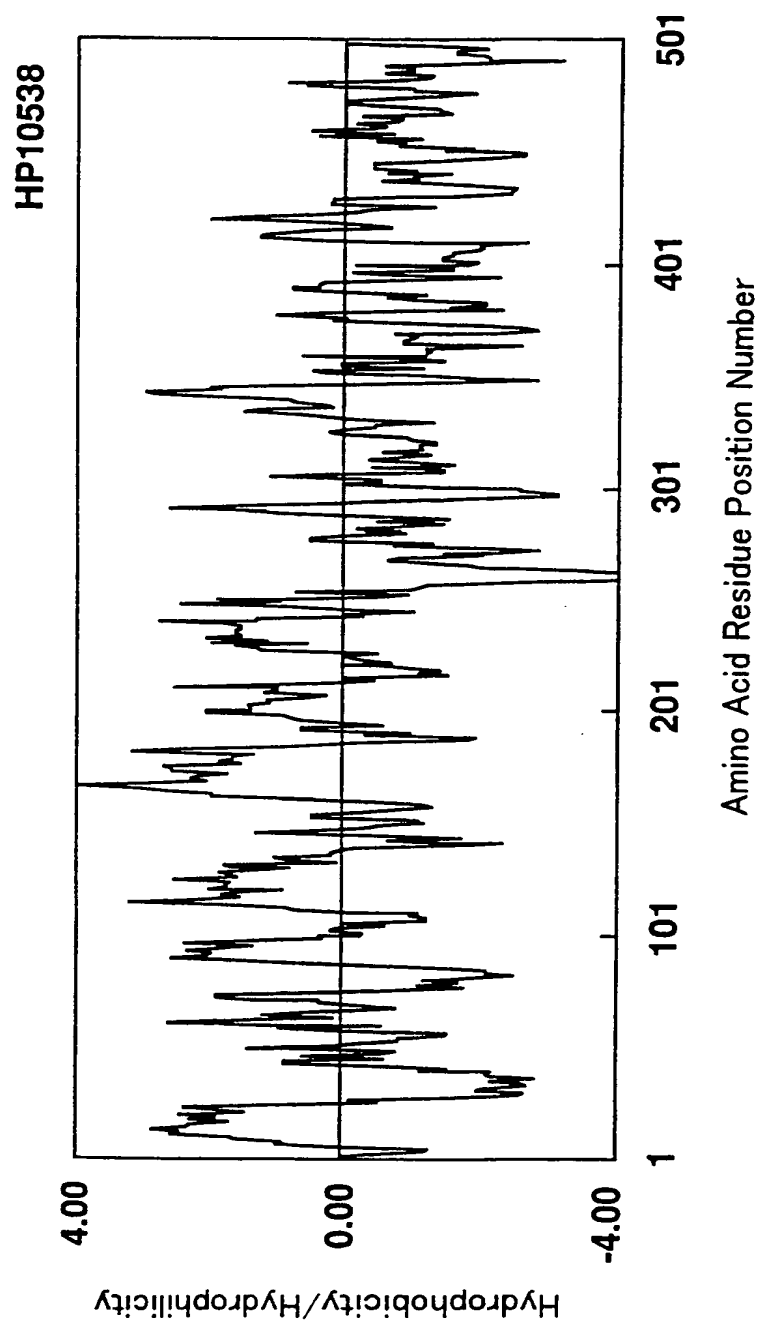


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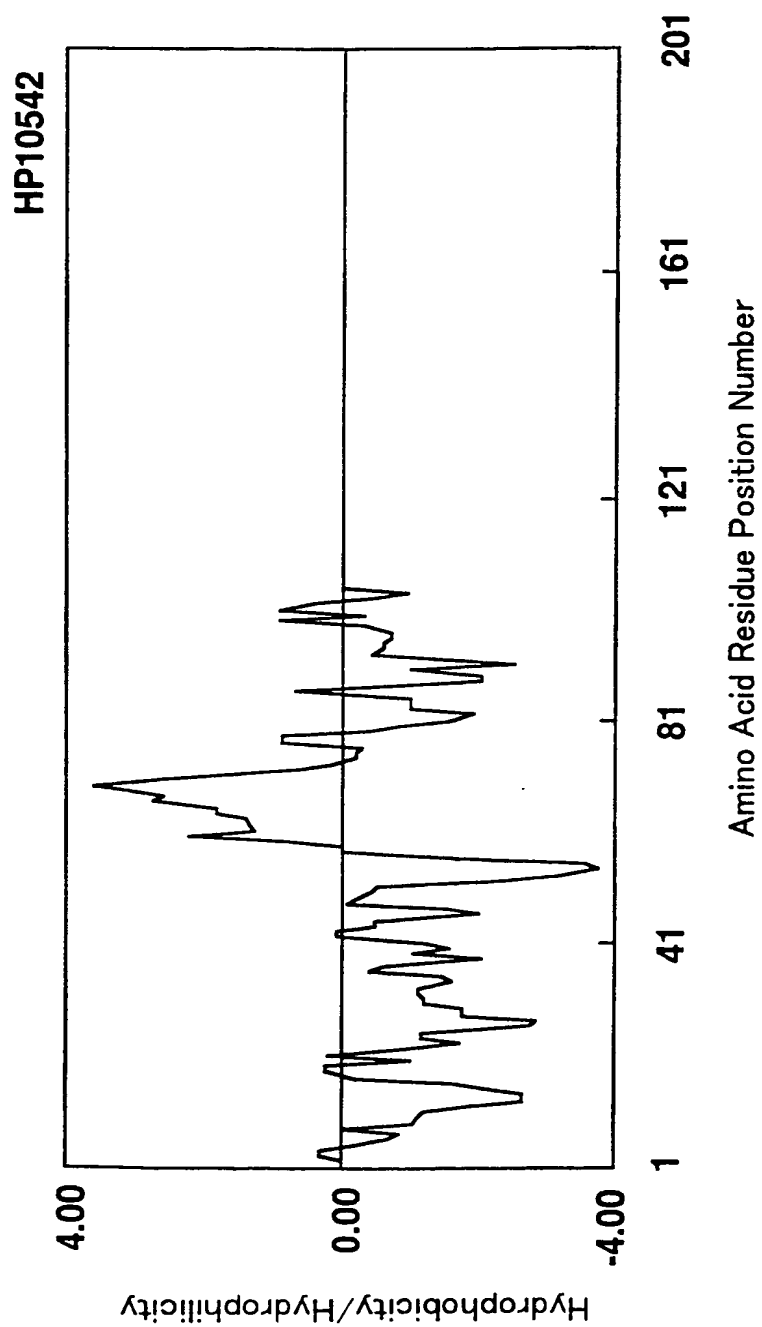


Fig. 29

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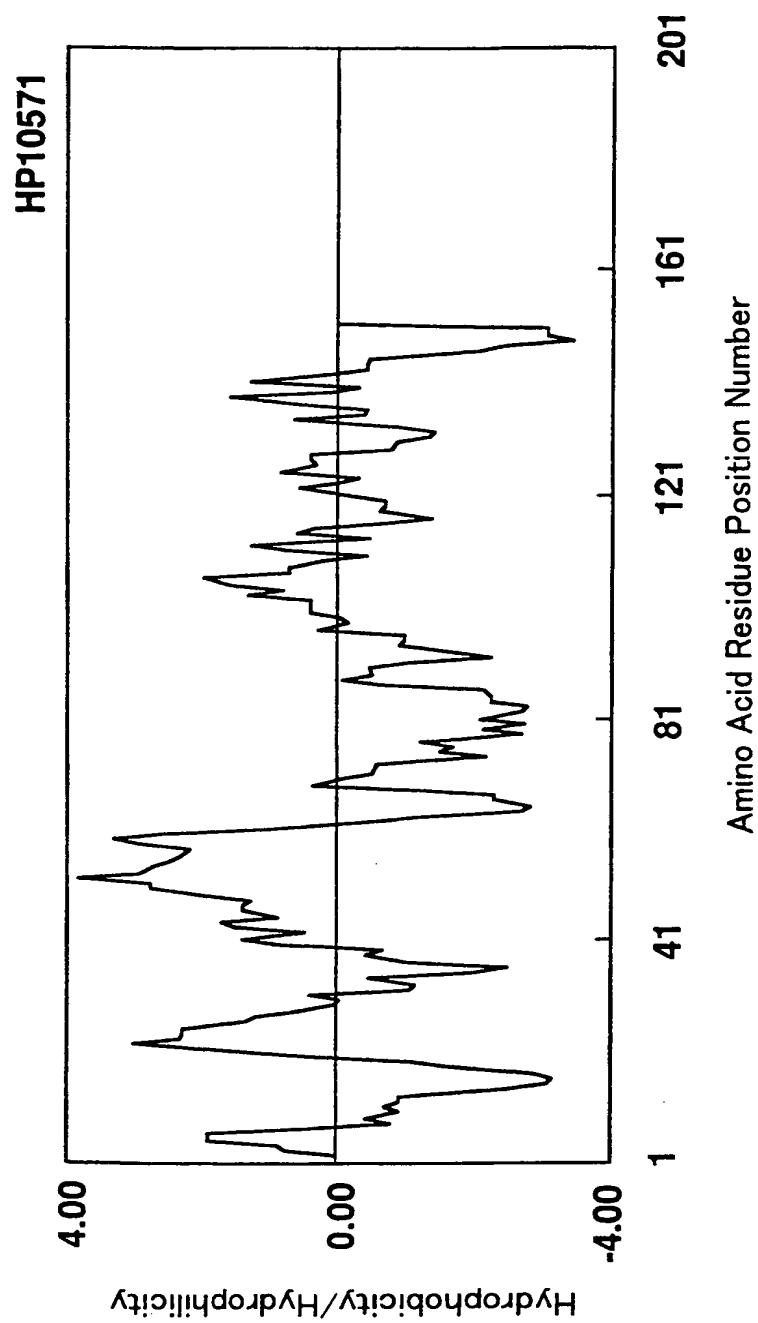


Fig. 30

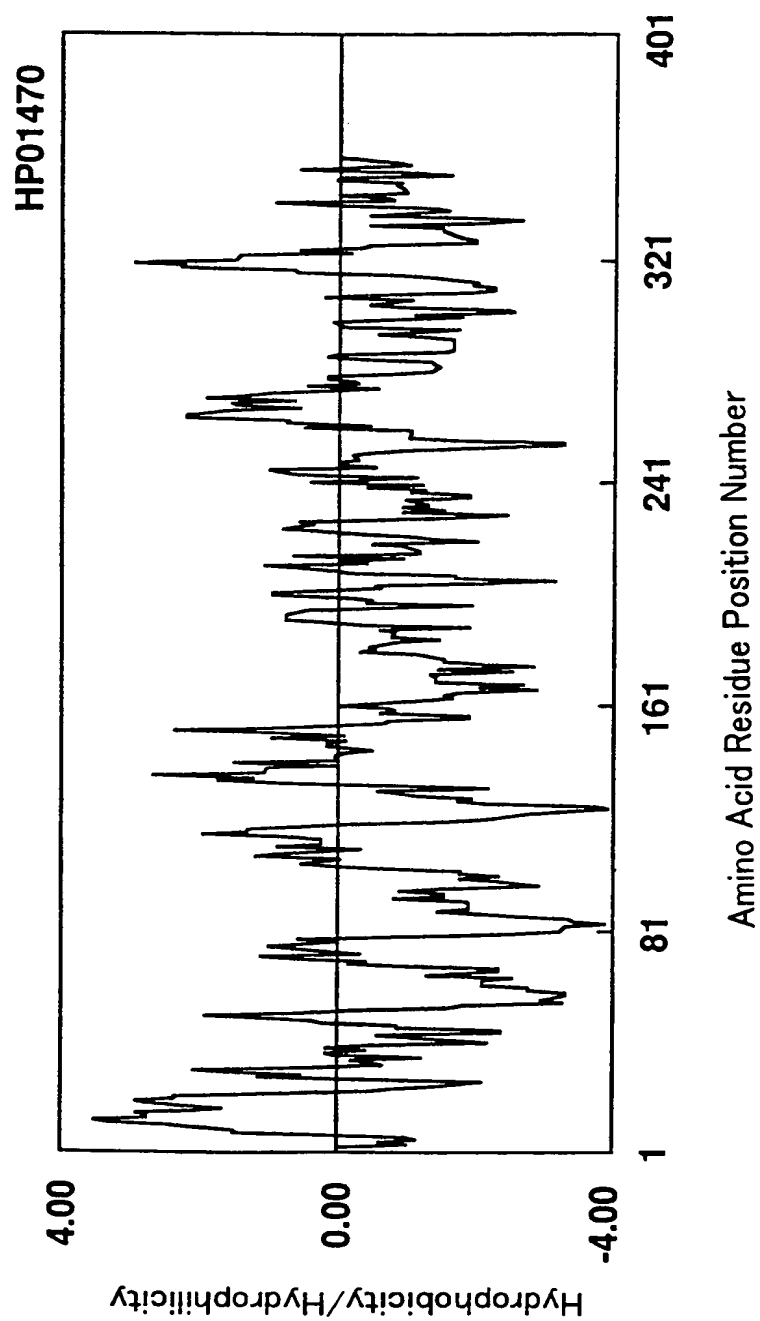


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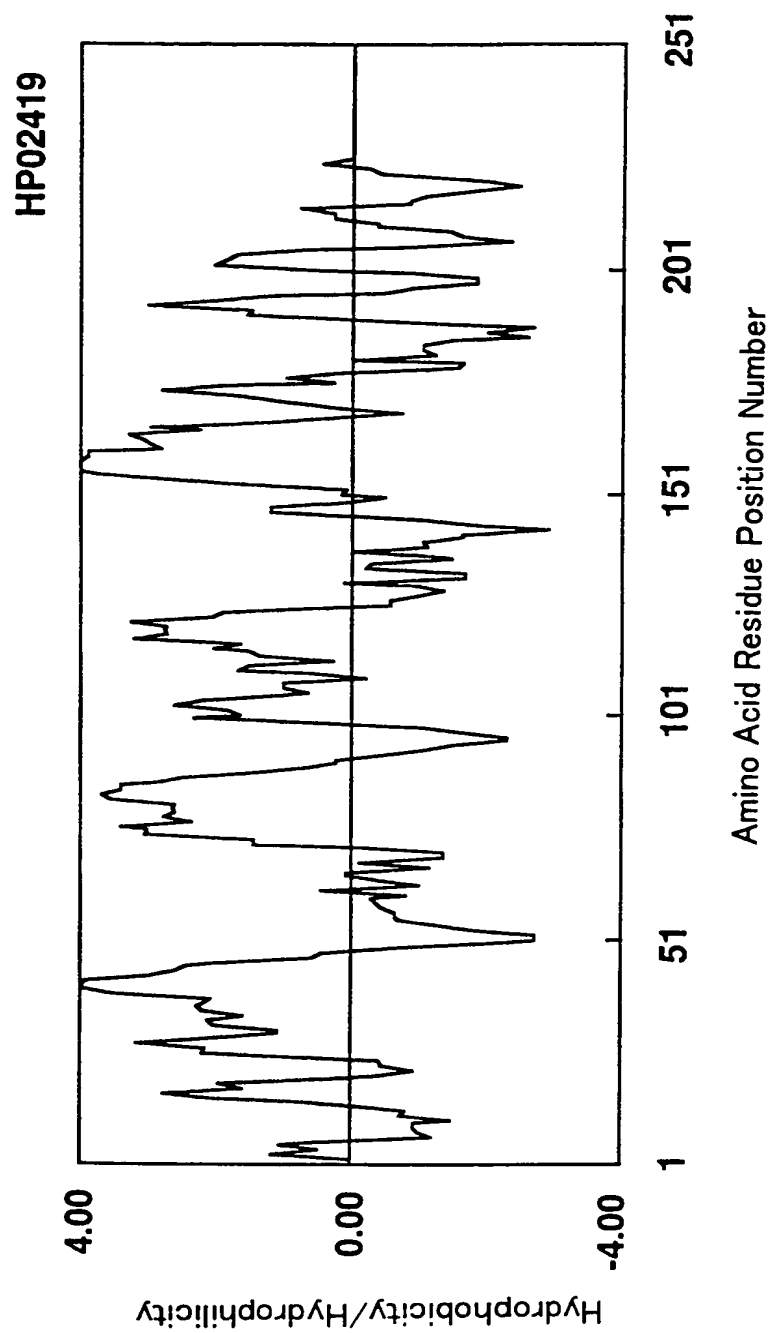


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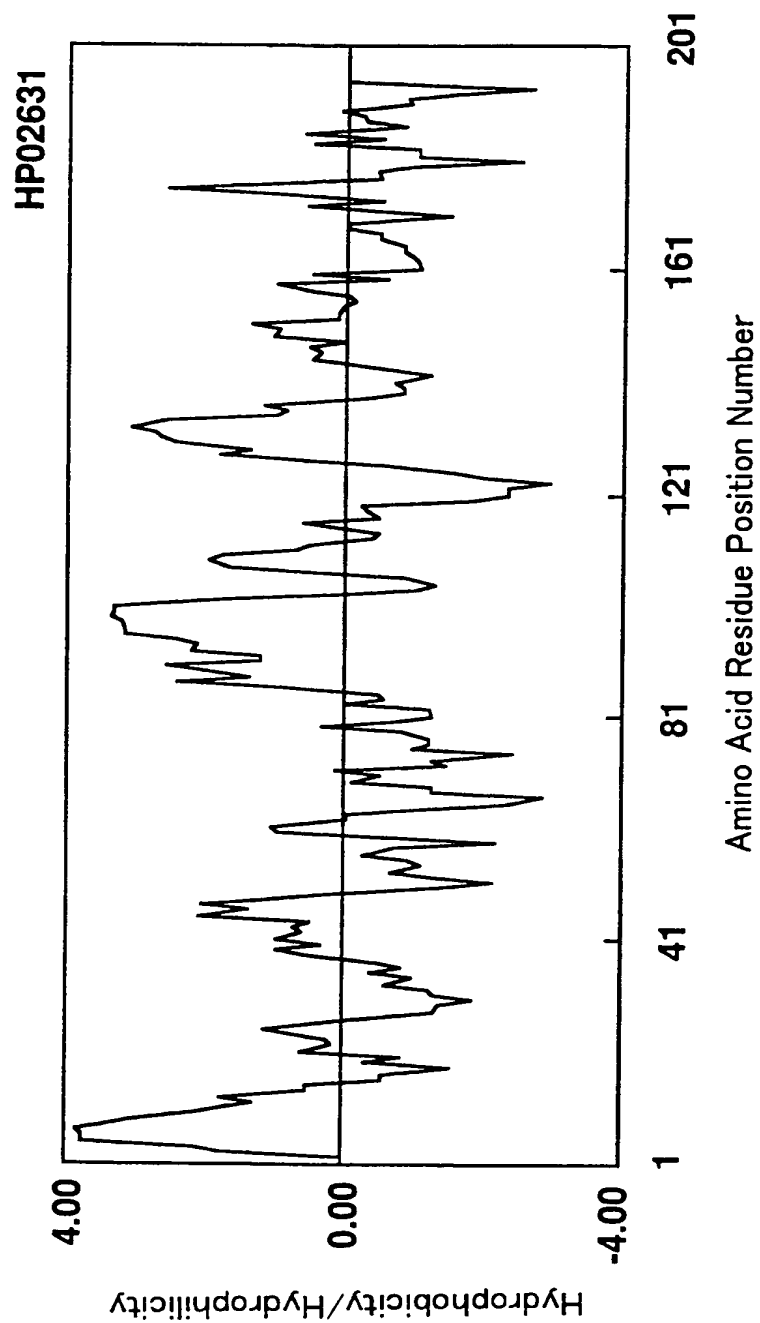


Fig. 33

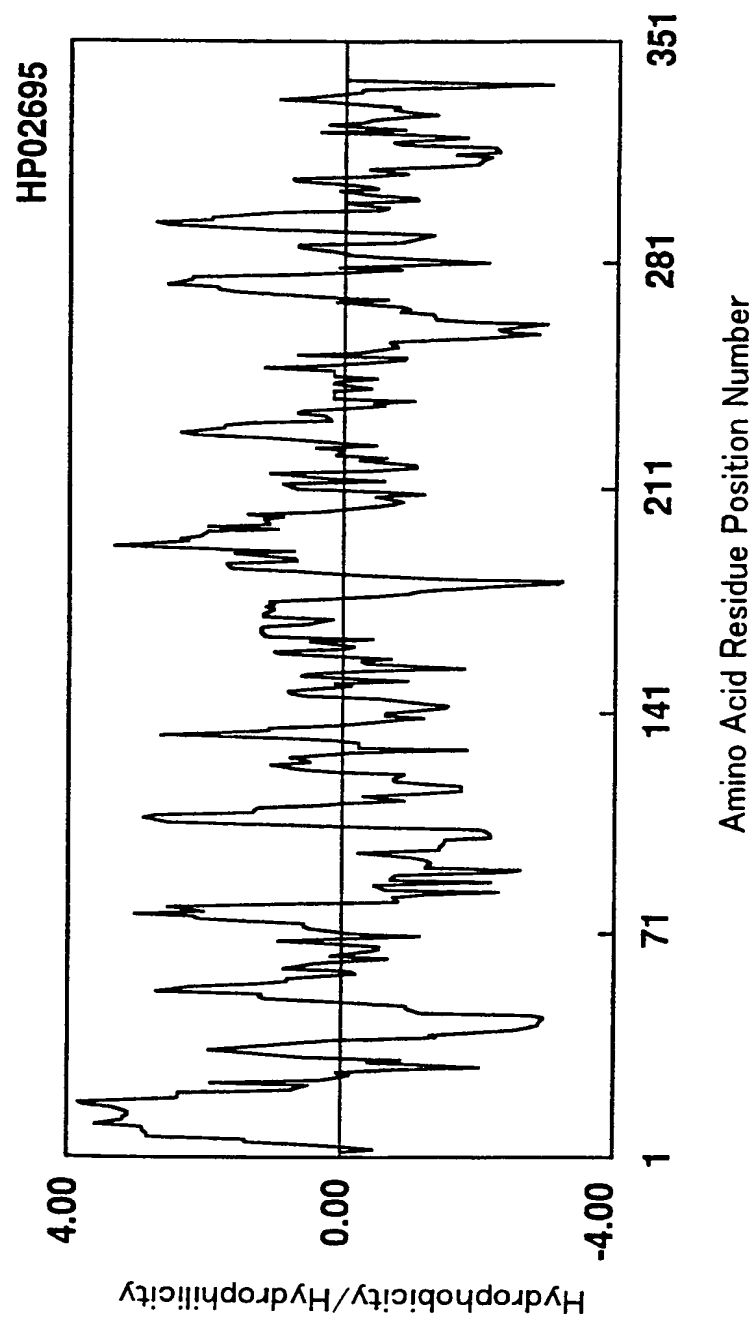


Fig. 34

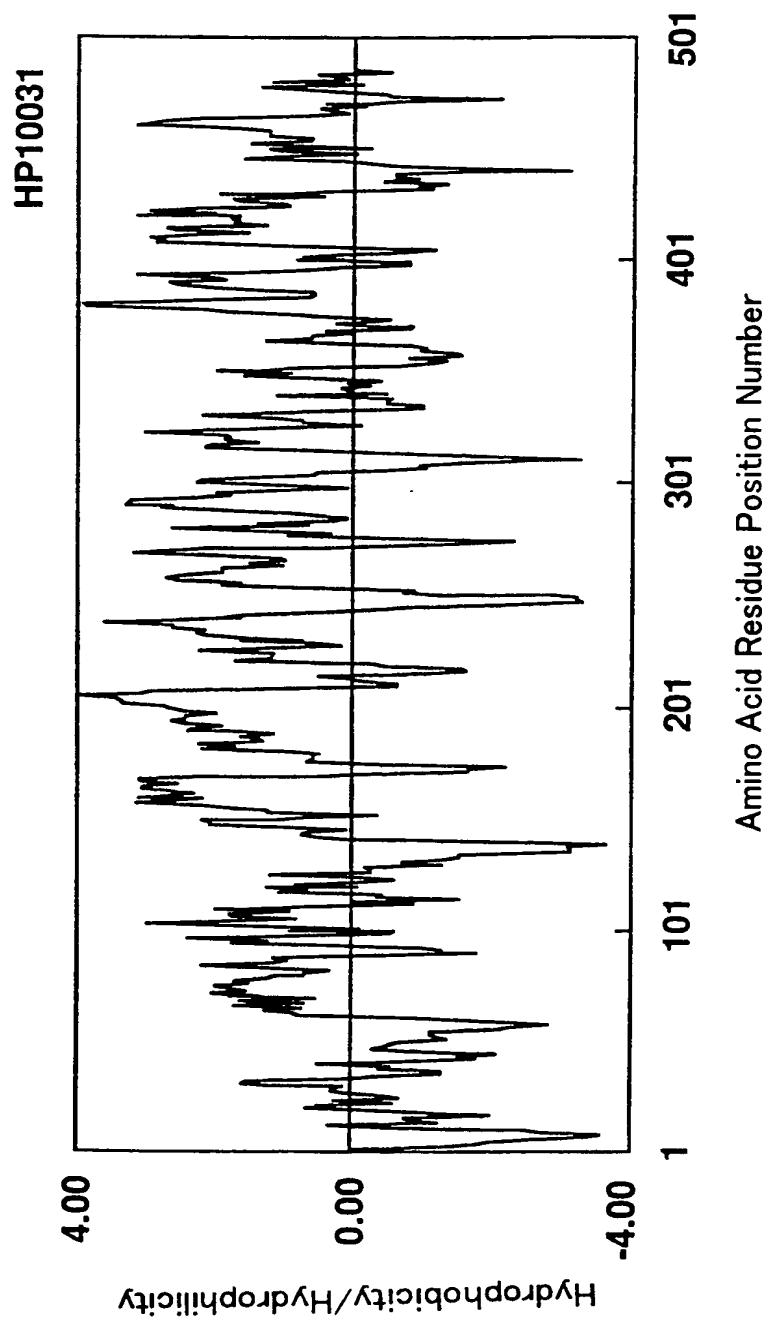


Fig. 35

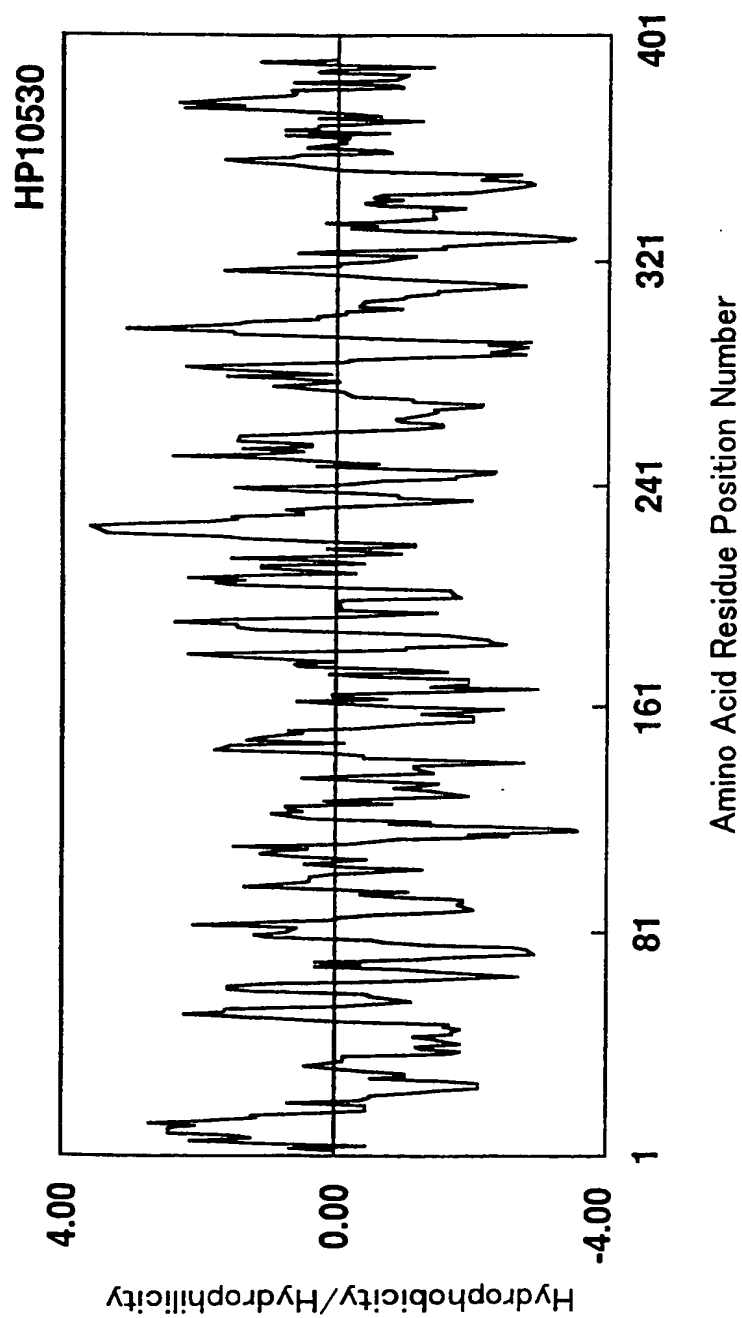


Fig. 36

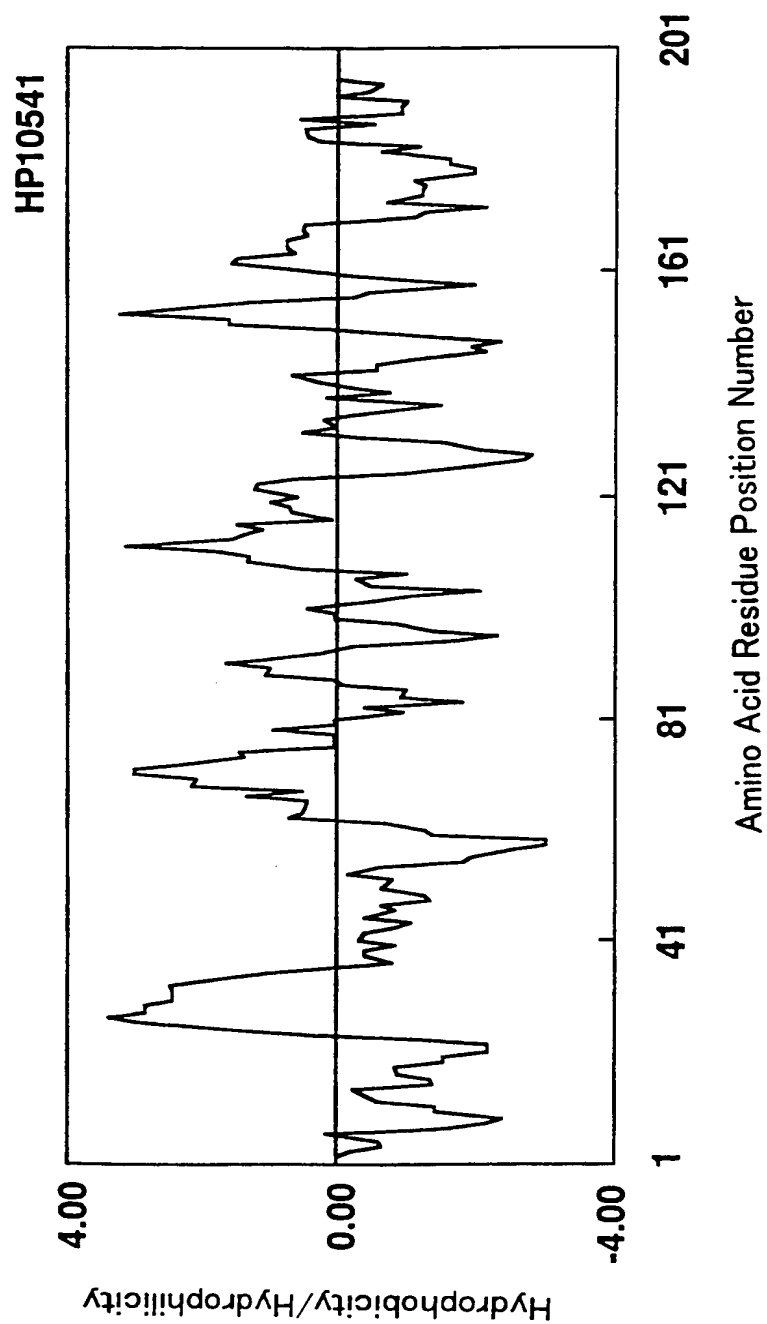


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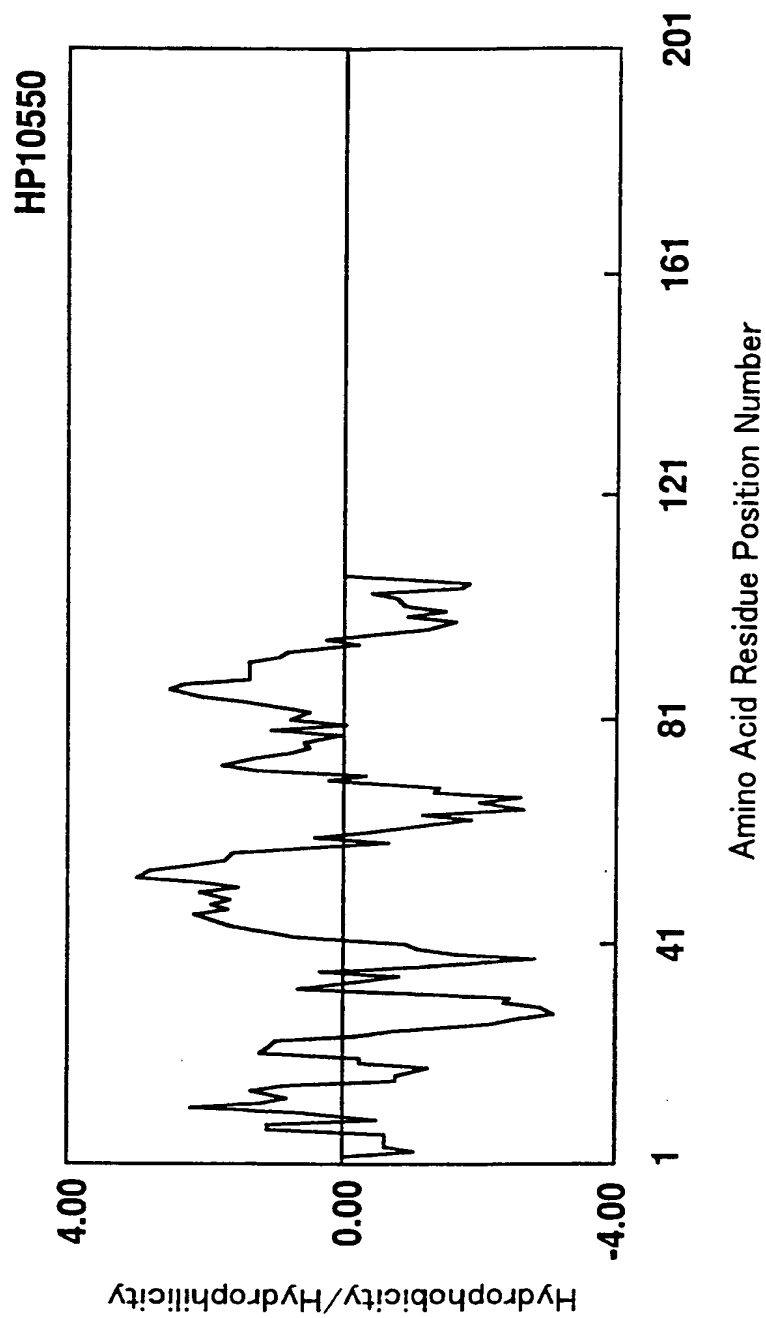


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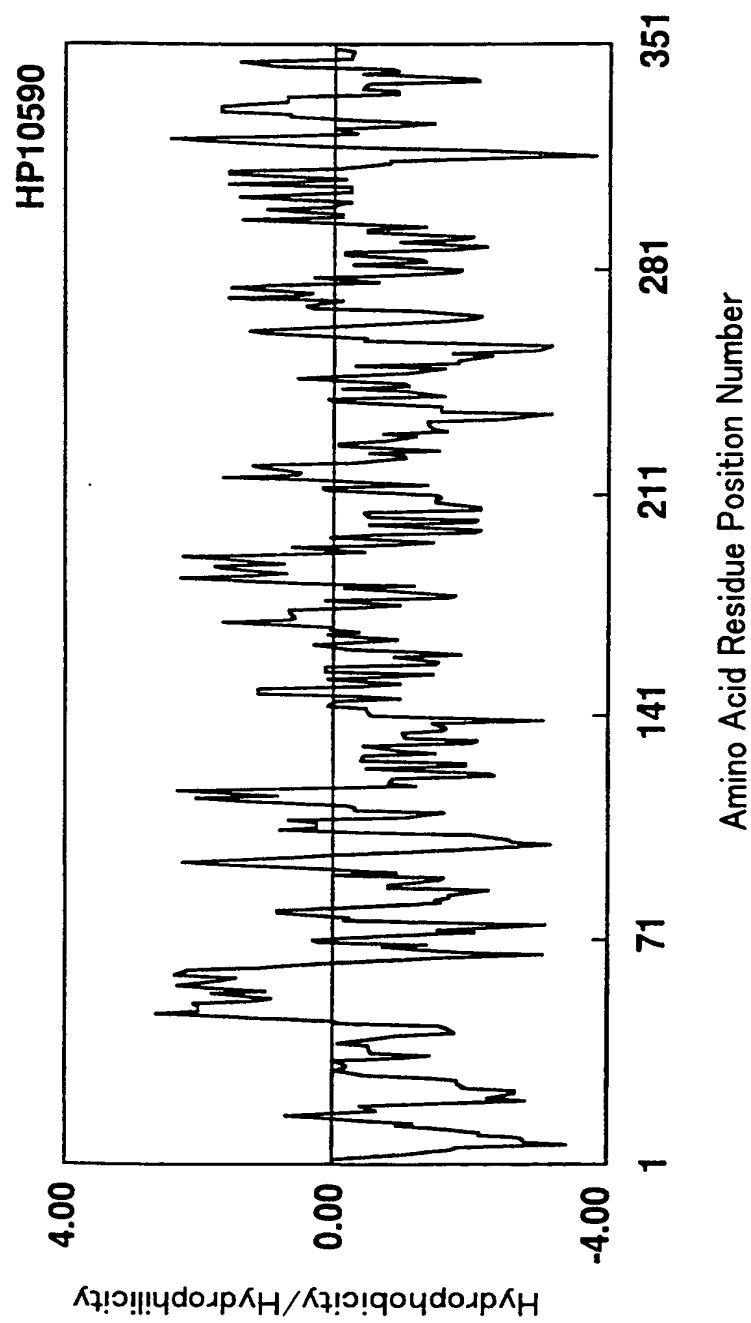


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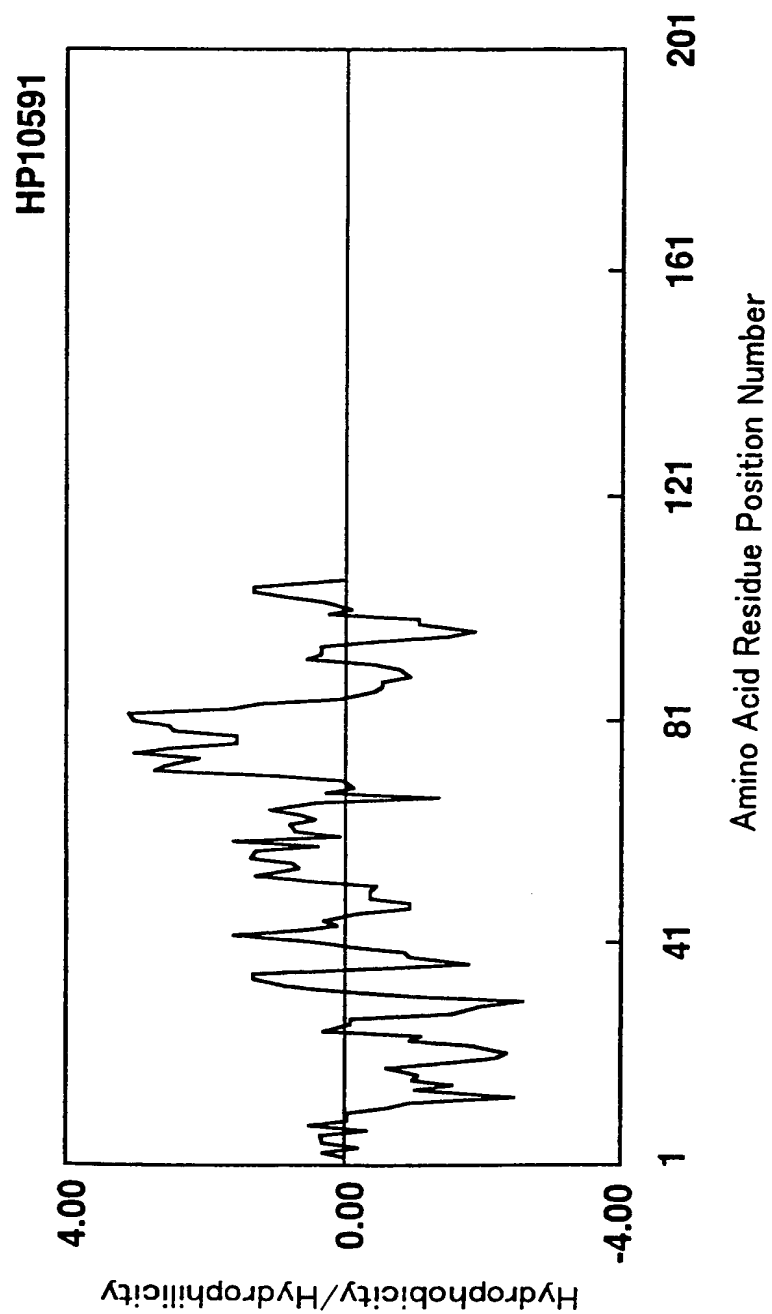


Fig. 40

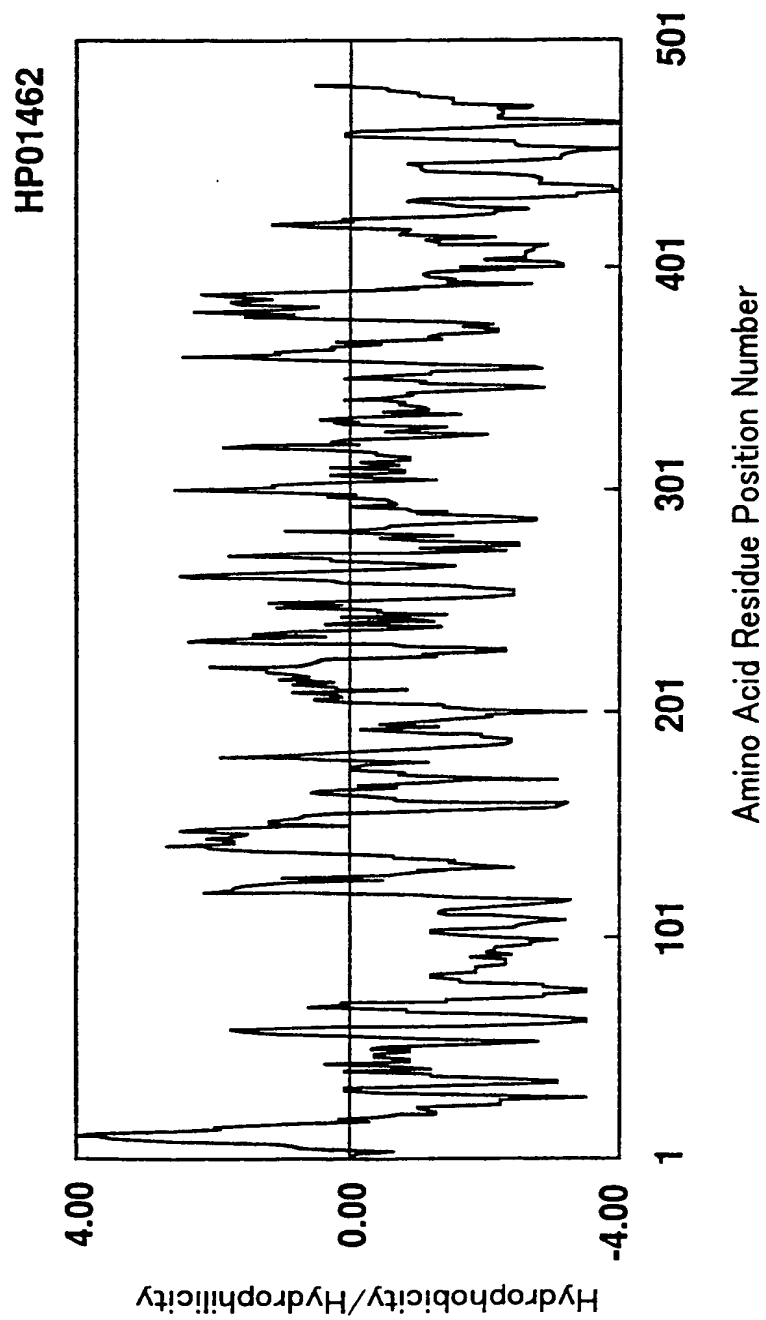


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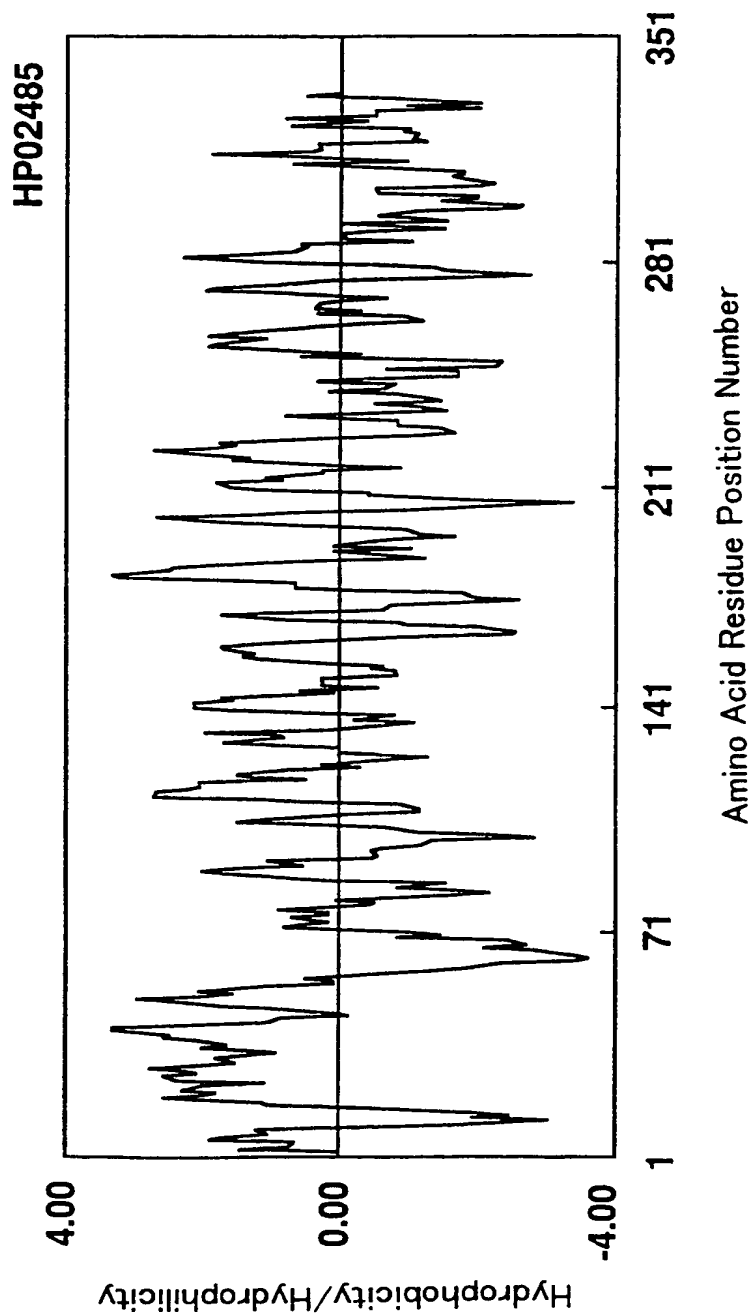


Fig.42

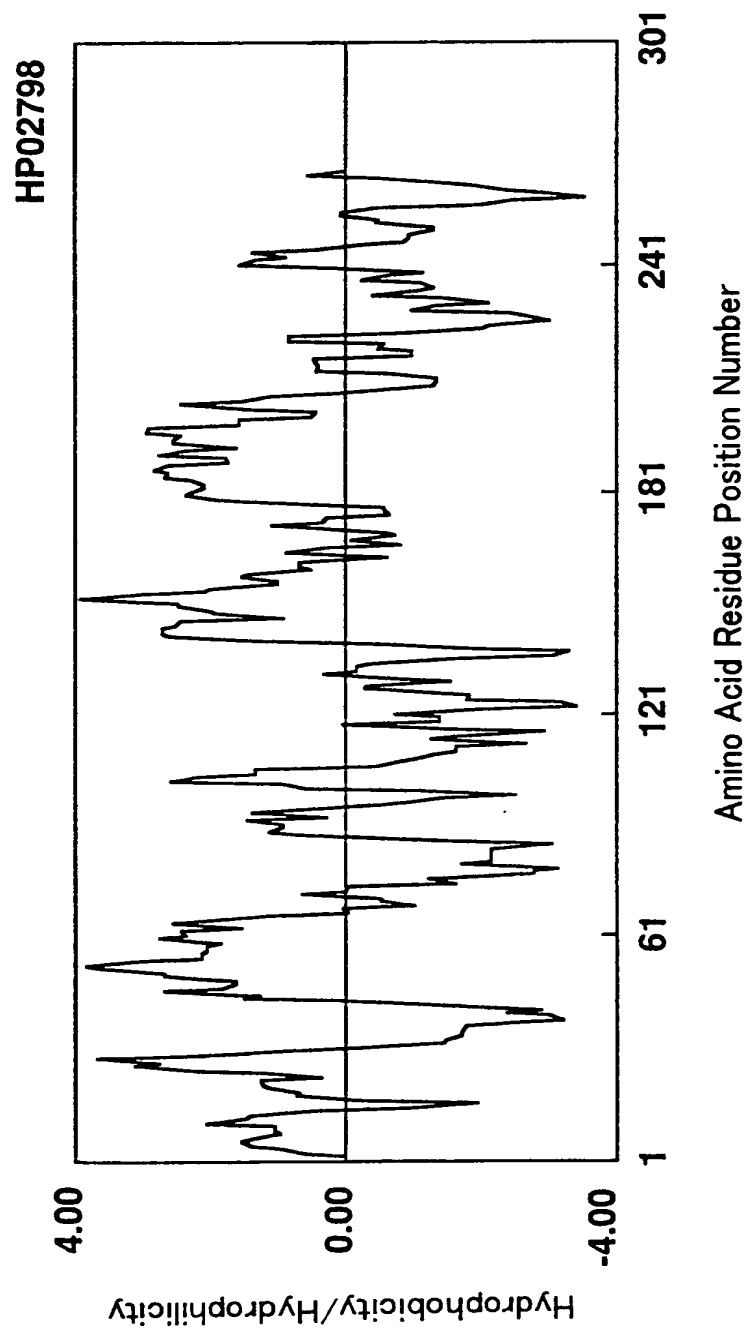


Fig. 43

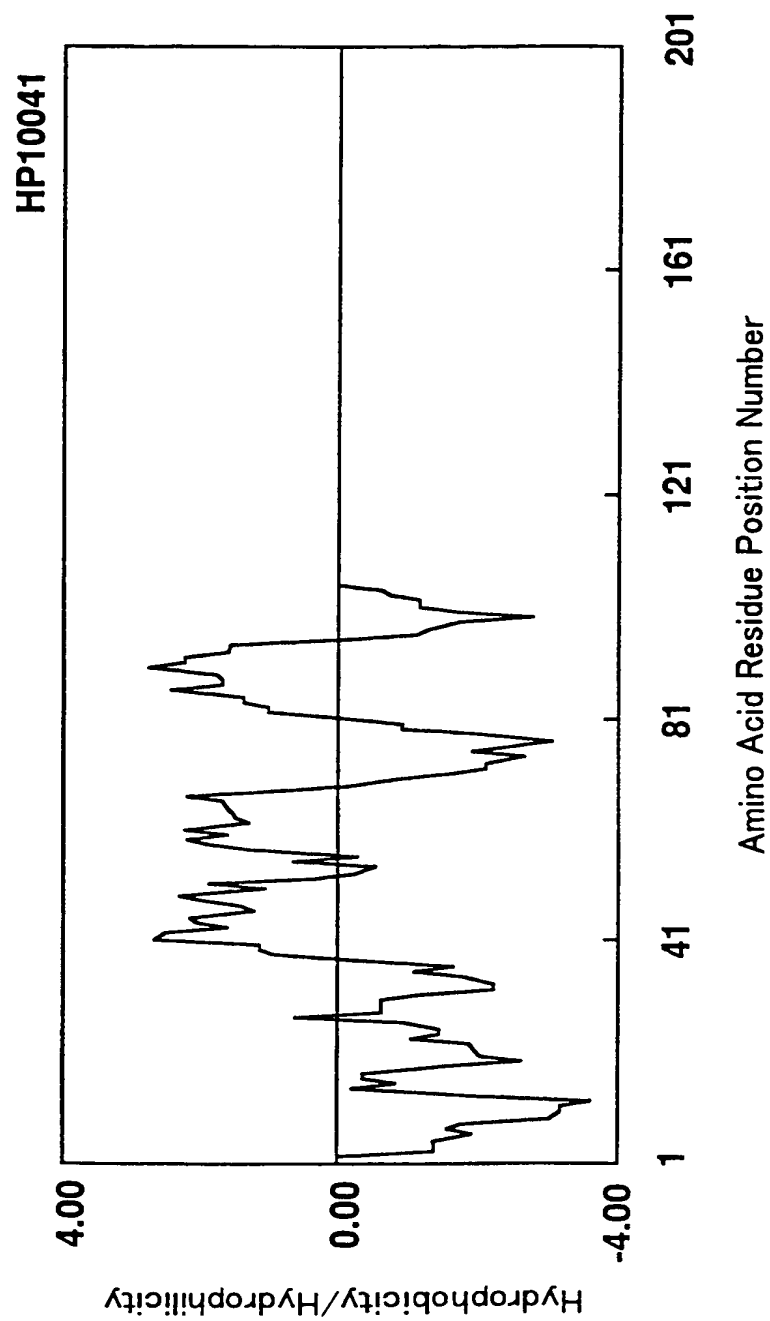


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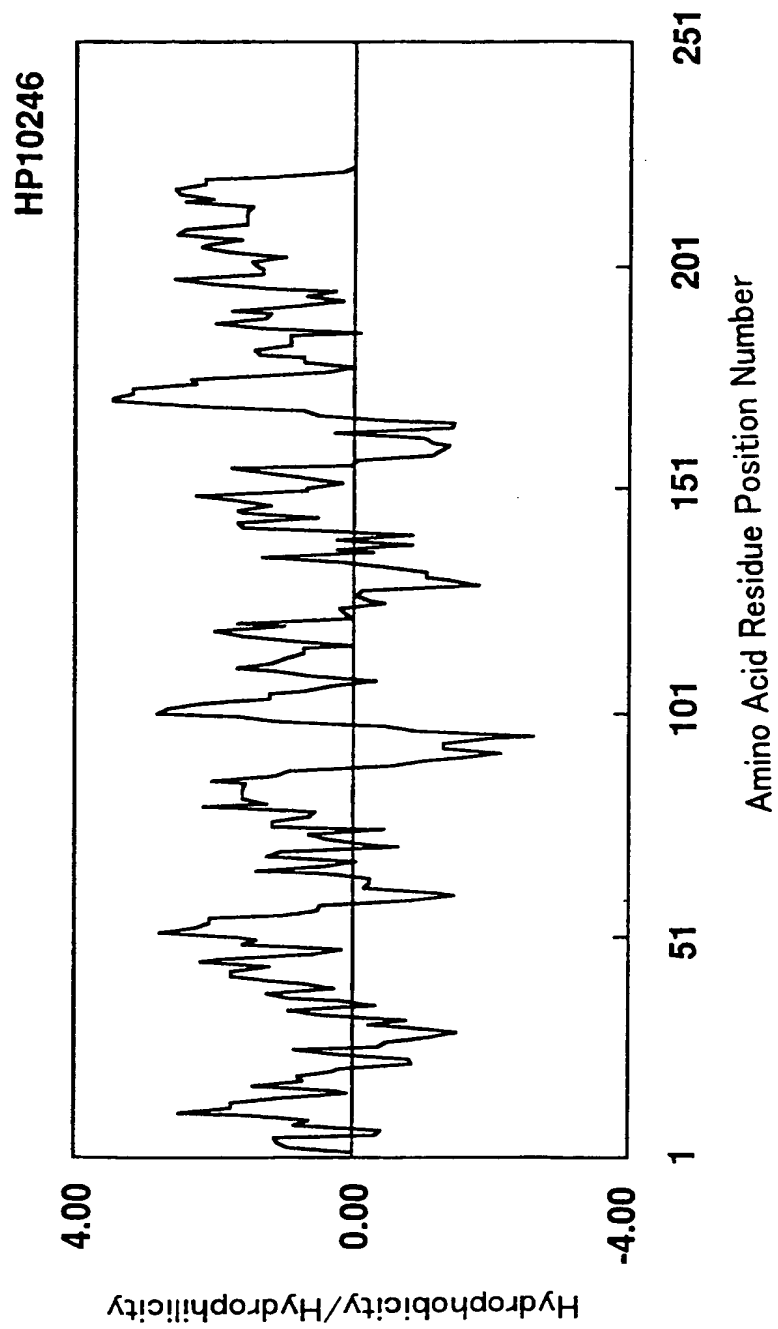


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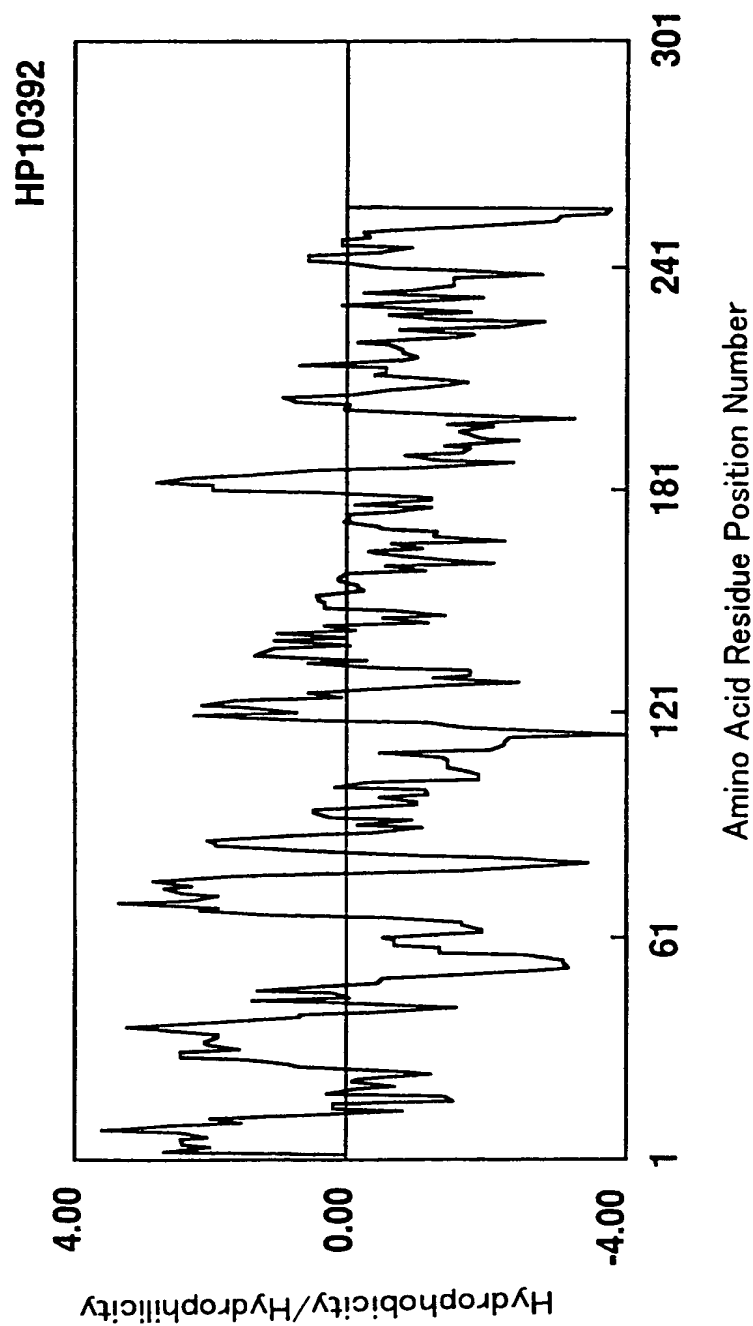


Fig. 46

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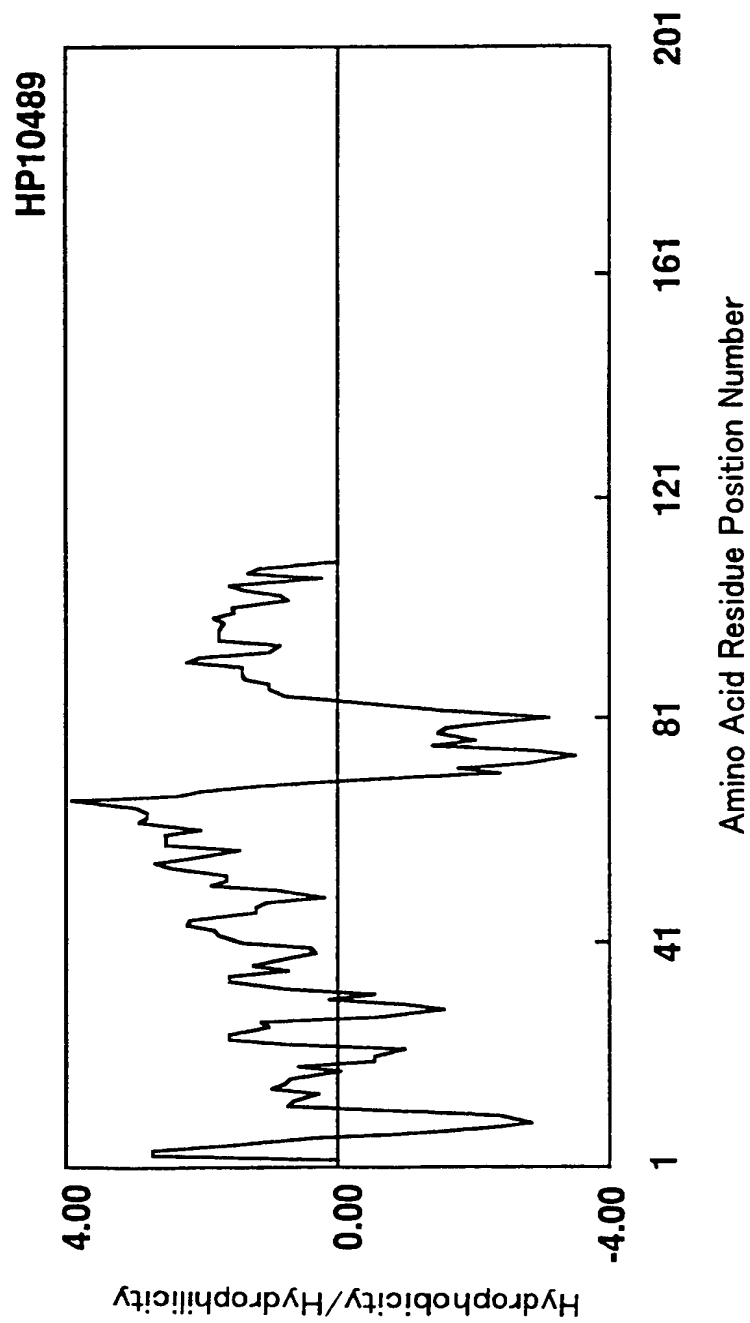


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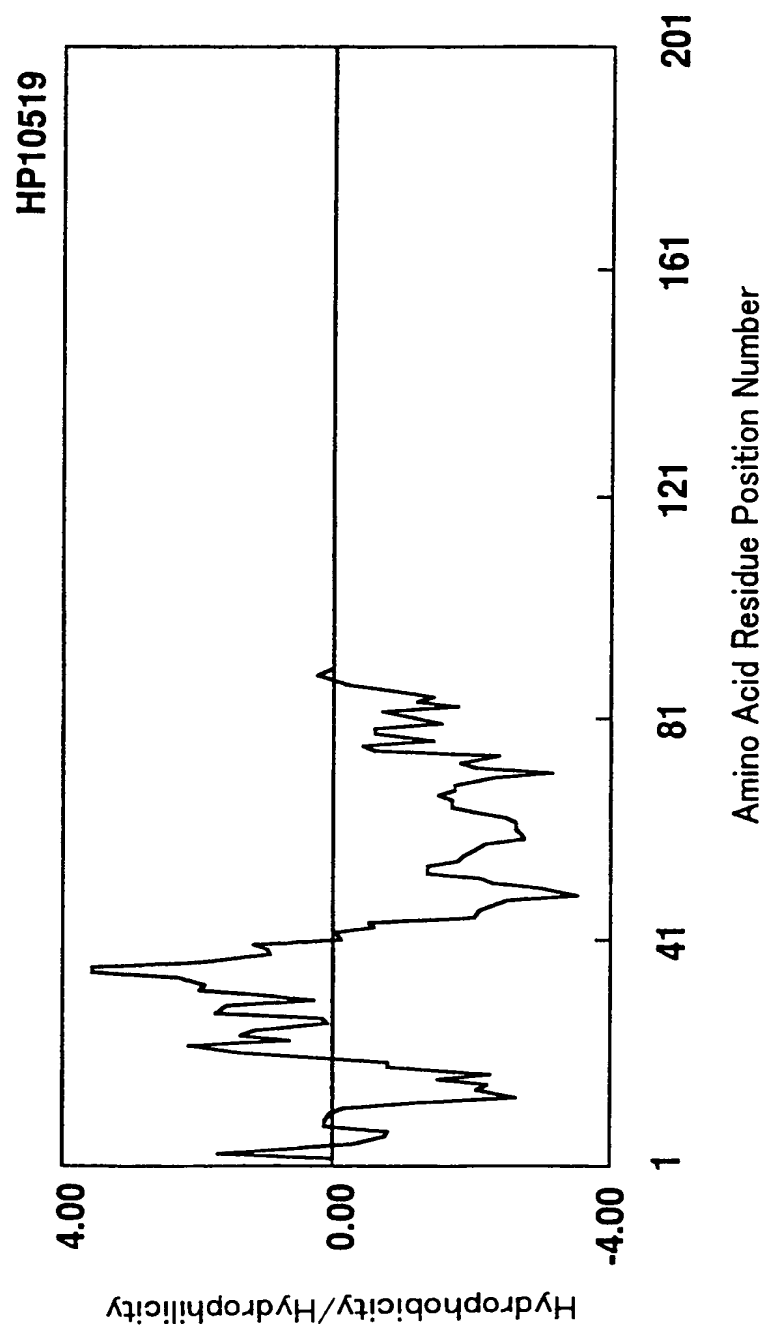


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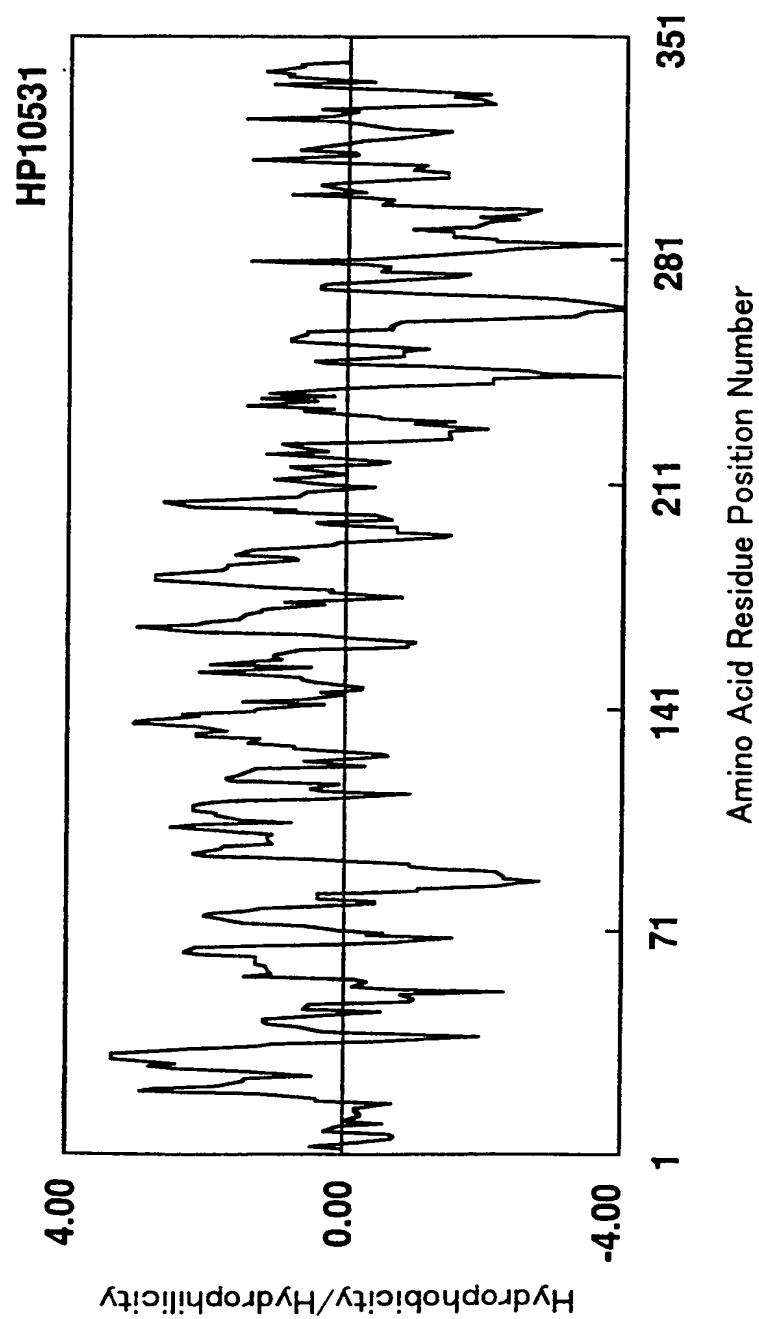


Fig. 49

50/50

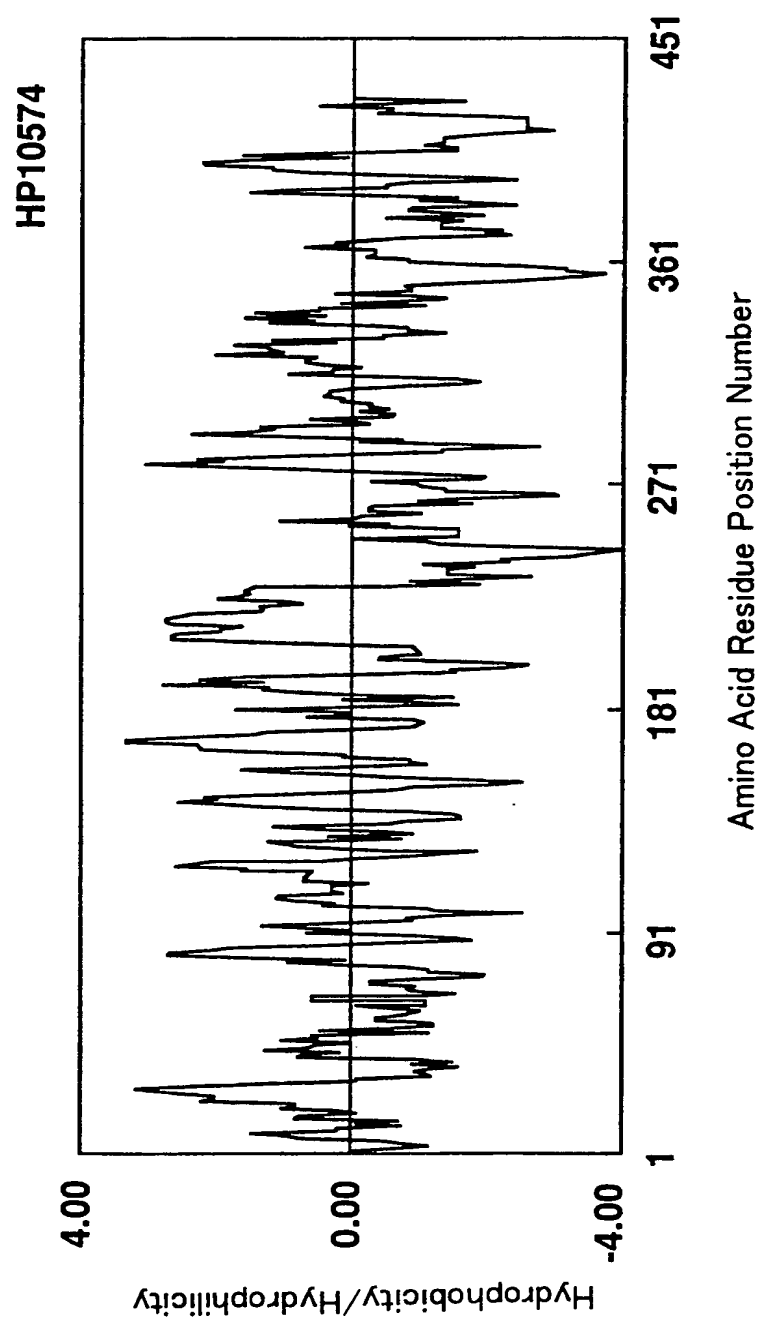


Fig. 50

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				20					25					30		
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				35				40					45			
	Tyr	Cys	Ile	Ala	Arg	Arg	Leu	Val	Asp	Asp	Thr	Asp	Ala	Met	Ser	Asn
30		50					55					60				
	Ala	Cys	Lys	Glu	Leu	Ala	Ile	Phe	Leu	Thr	Thr	Gly	Ile	Val	Val	Ser
	65					70					75					80
	Ala	Phe	Gly	Leu	Pro	Ile	Val	Phe	Ala	Arg	Ala	His	Leu	Ile	Glu	Trp
					85					90					95	
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 35 40 45
 Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile Ile Asp Pro Gly
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 Ser Thr Val Thr Val Ser Val Met Leu Gln Pro Phe Asp Tyr Asp Pro
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 Asn Glu Lys Ser Lys His Lys Phe Met Val Gln Thr Ile Phe Ala Pro
 85 90 95
 25 Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys Glu Ala Lys Pro Asp
 100 105 110
 Glu Leu Met Asp Ser Lys Leu Arg Cys Val Phe Glu Met Pro Asn Glu
 115 120 125
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 30 130 135 140
 Ala Ser Lys Gln Asp Gly Pro Met Pro Lys Pro His Ser Val Ser Leu
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20	Asp Leu Ile Ile Ser Thr Leu Asn Met Ser Lys Ile Gly Tyr Phe Tyr		
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	Thr Asp Cys Leu Val Pro Met Val Gly Asn Asn Pro Tyr Ala Thr Thr		
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	Glu Gly Asn Ser Thr Glu Leu Ser Ile Asn Ala Glu Val Tyr Ser Leu		
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	Pro Ser Arg Lys Leu Val Ala Leu Gln Leu Arg Ser Ile Phe Ile Lys		80
	85	90	95
	Tyr Lys Ser Lys Pro Phe Cys Glu Lys Leu Leu Ser Trp Val Lys Ser		
	100	105	110
30	Ser Gly Cys Ala Arg Val Ile Val Leu Ser Ser Ser His Ser Tyr Gln		
	115	120	125
	Arg Asn Asp Leu Gln Leu Arg Ser Thr Pro Phe Arg Tyr Leu Leu Thr		
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	Gly	Ala	Pro	Thr	Ser	Pro	Ala	Glu	His	Arg	Leu	Leu	Lys	Thr	Cys	Trp
			35					40					45			
	Ser	Cys	Arg	Val	Leu	Ser	Gly	Leu	Gly	Leu	Met	Gly	Ala	Gly	Gly	Tyr
		50					55					60				
30	Val	Tyr	Trp	Val	Ala	Arg	Lys	Pro	Met	Lys	Met	Gly	Tyr	Pro	Pro	Ser
	65					70					75					80
	Pro	Trp	Thr	Ile	Thr	Gln	Met	Val	Ile	Gly	Leu	Ser	Ile	Ala	Thr	Trp
				85						90					95	
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5 <213> Homo sapiens

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Pro Val Gln Glu Glu Lys Leu Ser Ala Ser Thr Ser Asn Leu Pro Cys
35 40 45
Trp Leu Val Glu Glu Phe Val Val Ala Glu Glu Cys Ser Pro Cys Ser
15 50 55 60
Asn Phe Arg Ala Lys Thr Thr Pro Glu Cys Gly Pro Thr Gly Tyr Val
65 70 75 80
Glu Lys Ile Thr Cys Ser Ser Ser Lys Arg Asn Glu Phe Lys Ser Cys
85 90 95
20 Arg Ser Ala Leu Met Glu Gln Arg Leu Phe Trp Lys Phe Glu Gly Ala
100 105 110
Val Val Cys Val Ala Leu Ile Phe Ala Cys Leu Val Ile Ile Arg Gln
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Arg Gln Leu Asp Arg Lys Ala Leu Glu Lys Val Arg Lys Gln Ile Glu
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Ser Ile
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	Ser	Lys	Thr	His
	Ser	Leu	Lys	Gly
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	Leu	Ala	Arg	Gly
	Gly	Ala	Gln	Ile
	Phe	Ser	Cys	Ile
	Ile	Pro	Glu	Cys
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	Leu	Gln	Arg	Ala
	Val	His	Gly	Leu
	Leu	His	Tyr	Leu
	Phe	His	Thr	Arg
	50	55	60	
	Asn	His	Thr	Phe
	Ile	Val	Leu	His
	Leu	Val	Leu	Gln
	Gly	Met	Val	Tyr
	65	70	75	80
10	Thr	Glu	Tyr	Thr
	Trp	Glu	Val	Phe
	Gly	Tyr	Cys	Gln
	Glu	Leu	Glu	Leu
	85	90	95	
	Ser	Leu	His	Tyr
	Leu	Leu	Leu	Pro
	Tyr	Leu	Leu	Gly
	Val	Asn	Leu	
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	Phe	Phe	Phe	Thr
	Leu	Thr	Cys	Gly
	Thr	Asn	Pro	Gly
	Ile	Ile	Thr	Lys
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	Ala	Asn	Glu	Leu
	Leu	Phe	Leu	His
	Val	Tyr	Glu	Phe
	Asp	Glu	Val	Met
	130	135	140	
	Phe	Pro	Lys	Asn
	Val	Arg	Cys	Ser
	Thr	Cys	Asp	Leu
	Arg	Lys	Pro	Ala
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	Asn	Trp	Cys	Val
	His	Arg	Phe	Asp
	165	170	175	
	His	His	Cys	Val
	Trp	Val	Asn	Asn
	Cys	Ile	Gly	Ala
	Trp	Asn	Ile	Arg
	180	185	190	
	Tyr	Phe	Leu	Ile
	Tyr	Val	Leu	Thr
	Leu	Thr	Ala	Ser
	Ala	Ala	Thr	Val
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	Ala	Ile	Val	Ser
	Thr	Thr	Phe	Leu
	Val	His	Leu	Val
	Val	Met	Ser	Asp
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	Leu	Tyr	Gln	Glu
	Thr	Tyr	Ile	Asp
	Asp	Leu	Gly	His
	Leu	His	Val	Met
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	Leu	Ile	Gln	Tyr
	Leu	Phe	Leu	Thr
	Phe	Pro	Arg	Ile
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	Val	Phe	Met	Leu
	Gly	Phe	Val	Val
	Val	Leu	Ser	Phe
	Leu	Gly	Gly	
	260	265	270	
	Tyr	Leu	Leu	Phe
	Val	Leu	Tyr	Leu
	Ala	Ala	Thr	Asn
	Gln	Thr	Thr	Asn
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 Ala Trp Pro Pro Ser Ala Glu Pro Gln Val His Arg Asn Ile His Ser
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 Cys His Glu Arg Lys Lys Gln Glu
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 35 40 45
 Leu Glu Lys Glu Lys Asn Ser Leu Met Asn Lys Ala Ser Asn Tyr Glu
 50 55 60
 Lys Glu Leu Lys Phe Leu Arg Gln Glu Asn Arg Lys Asn Met Leu Leu
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 Leu Asn Lys Asn Leu Phe Asp Asn Leu Ile Glu Phe Leu Gln Lys Ser
 10 65 70 75 80
 His Ser Gly Phe Gln Lys Asn Ser Arg Asp Leu Gly Gly Gln Ile Lys
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 Gly Lys Pro Ile Ser Glu Ser His Pro Ile Leu Tyr Phe Thr Asn Gly
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 His Leu Tyr Pro Thr Gly Ser Lys Ser Lys Arg Val Ser Leu Leu Gln
 35 85 90 95

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Asn Pro Pro Thr Val Gly Val Ala Thr Leu Lys Leu Thr Asp Val His
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Pro Ser Asn Pro Leu Cys Ser Gln Ser Gly Gln Thr Ser Val Gly Gly
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Ser Thr Ala Leu Arg Cys Ser Ser Ser Glu Gly Ala Pro Lys Pro Val
10 165 170 175
Tyr Asn Trp Val Arg Leu Gly Thr Phe Pro Thr Pro Ser Pro Gly Ser
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Met Val Gln Asp Glu Val Ser Gly Gln Leu Ile Leu Thr Asn Leu Ser
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15 Leu Thr Ser Ser Gly Thr Tyr Arg Cys Val Ala Thr Asn Gln Met Gly
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Ser Ala Ser Cys Glu Leu Thr Leu Ser Val Thr Glu Pro Ser Gln Gly
225 230 235 240
Arg Val Ala Gly Ala Leu Ile Gly Val Leu Leu Gly Val Leu Leu Leu
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Ser Val Ala Ala Phe Cys Leu Val Arg Phe Gln Lys Glu Arg Gly Lys
260 265 270
Lys Pro Lys Glu Thr Tyr Gly Gly Ser Asp Leu Arg Glu Asp Ala Ile
275 280 285
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	<221> CDS	
35	<222> (66)...(443)	

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<400> 21

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5 Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met Gly Val Gln Val

1 5 10 15

gtg ggc agg gcc ttt gca cgg gcc ttg cgg cag gag ttt gca gcc agc 158

Val Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu Phe Ala Ala Ser

20 25 30

10 cgg gcc gca gct gat gcc cga gga cgc gct gga cac cgg tct gca gcc 206

Arg Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His Arg Ser Ala Ala

35 40 45

gct tcc aac ctc tcc ggc ctc agc ctc cag gag gca cag cag att ctc 254

Ala Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala Gln Gln Ile Leu

15 50 55 60

aac gtg tcc aag ctg agc cct gag gag gtc cag aag aac tat gaa cac 302

Asn Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys Asn Tyr Glu His

65 70 75

tta ttt aag gtg aat gat aaa tcc gtg ggt ggc tcc ttc tac ctg cag 350

20 Leu Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser Phe Tyr Leu Gln

80 85 90 95

tca aag gtg gtc cgc gca aag gag cgc ctg gat gag gaa ctc aaa atc 398

Ser Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu Glu Leu Lys Ile

100 105 110

25 cag gcc cag gag gac aga gaa aaa ggg cag atg ccc cat acg tgactgctc 450

Gln Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro His Thr

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30 <210> 22

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35 <221> CDS

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<222> (104)...(499)

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	Met Ala Gly Ile	
	1	
	aaa gct ttg att agt ttg tcc ttt gga gga gca atc gga ctg atg ttt	163
	Lys Ala Leu Ile Ser Leu Ser Phe Gly Gly Ala Ile Gly Leu Met Phe	
10	5 10 15 20	
	ttg atg ctt gga tgt gcc ctt cca ata tac aac aaa tac tgg ccc ctc	211
	Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr Asn Lys Tyr Trp Pro Leu	
	25 30 35	
	ttt gtt cta ttt ttt tac atc ctt tca cct att cca tac tgc ata gca	259
15	Phe Val Leu Phe Phe Tyr Ile Leu Ser Pro Ile Pro Tyr Cys Ile Ala	
	40 45 50	
	aga aga tta gtg gat gat aca gat gct atg agt aac gct tgt aag gaa	307
	Arg Arg Leu Val Asp Asp Thr Asp Ala Met Ser Asn Ala Cys Lys Glu	
	55 60 65	
20	ctt gcc atc ttt ctt aca acg ggc att gtc gtg tca gct ttt gga ctc	355
	Leu Ala Ile Phe Leu Thr Thr Gly Ile Val Val Ser Ala Phe Gly Leu	
	70 75 80	
	cct att gta ttt gcc aga gca cat ctg att gag tgg gga gct tgt gca	403
	Pro Ile Val Phe Ala Arg Ala His Leu Ile Glu Trp Gly Ala Cys Ala	
25	85 90 95 100	
	ctt gtt ctc aca gga aac aca gtc atc ttt gca act ata cta ggc ttt	451
	Leu Val Leu Thr Gly Asn Thr Val Ile Phe Ala Thr Ile Leu Gly Phe	
	105 110 115	
	ttc ttg gtc ttt gga agc aat gac gac ttc agc tgg cag cag tgg tgaa	500
30	Phe Leu Val Phe Gly Ser Asn Asp Asp Phe Ser Trp Gln Gln Trp	
	120 125 130	
	aagaaattac tgaactattg tcaaattggac ttctgtcat ttgttgcca ttcacgcaca	560
	caggagatgg ggcagttaat gctgaatggg atagcaagcc tcttgggggg attttaggtg	620
	ctcccttctc acttttattg taagcatact attttcacag agacttgetg aaggattaaa	680
35	aggattttct cttttgg	697

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 tggggttgag tcagttgtgg gacccggagc tgetgacca gcgggtggcc caccgaaccg 120
 gtgacacagc ggcaggcggt agggctcggg agccgcgagc ctggcctcgt cctagagetc 180
 ggccgagccg tcgccgccgt cgteccccgc cccagtcag caaacgccg ccgcgggcgc 240
 15 gccccgctc tgcgtgtct ctccgatggc gtccgcctca ggggcc atg gcg aag 295
 Met Ala Lys
 1
 cac gag cag atc ctg gtc ctc gat ccg ccc aca gac ctc aaa ttc aaa 343
 His Glu Gln Ile Leu Val Leu Asp Pro Pro Thr Asp Leu Lys Phe Lys
 20 5 10 15
 ggc ccc ttc aca gat gta gtc act aca aat ctt aaa ttg cga aat cca 391
 Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu Lys Leu Arg Asn Pro
 20 25 30 35
 tcg gat aga aaa gtg tgt ttc aaa gtg aag act aca gca cct cgc cgg 439
 25 Ser Asp Arg Lys Val Cys Phe Lys Val Lys Thr Thr Ala Pro Arg Arg
 40 45 50
 tac tgt gtg agg ccc aac agt gga att att gac cca ggg tca act gtg 487
 Tyr Cys Val Arg Pro Asn Ser Gly Ile Ile Asp Pro Gly Ser Thr Val
 55 60 65
 30 act gtt tca gta atg cta cag ccc ttt gac tat gat ccg aat gaa aag 535
 Thr Val Ser Val Met Leu Gln Pro Phe Asp Tyr Asp Pro Asn Glu Lys
 70 75 80
 agt aaa cac aag ttt atg gta cag aca att ttt gct cca cca aac act 583
 Ser Lys His Lys Phe Met Val Gln Thr Ile Phe Ala Pro Pro Asn Thr
 35 85 90 95

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	tca gat atg gaa gct gtg tgg aaa gag gca aaa cct gat gaa tta atg	631
	Ser Asp Met Glu Ala Val Trp Lys Glu Ala Lys Pro Asp Glu Leu Met	
	100 105 110 115	
	gat tcc aaa ttg aga tgc gta ttt gaa atg ccc aat gaa aat gat aaa	679
5	Asp Ser Lys Leu Arg Cys Val Phe Glu Met Pro Asn Glu Asn Asp Lys	
	120 125 130	
	ttg aat gat atg gaa cct agc aaa gct gtt cca ctg aat gca tct aag	727
	Leu Asn Asp Met Glu Pro Ser Lys Ala Val Pro Leu Asn Ala Ser Lys	
	135 140 145	
10	caa gat gga cct atg cca aaa cca cac agt gtt tca ctt aat gat acc	775
	Gln Asp Gly Pro Met Pro Lys Pro His Ser Val Ser Leu Asn Asp Thr	
	150 155 160	
	gaa aca agg aaa cta atg gaa gag tgt aaa aga ctt cag gga gaa atg	823
	Glu Thr Arg Lys Leu Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Met	
15	165 170 175	
	atg aag cta tca gaa gaa aat cgg cac ctg aga gat gaa ggt tta agg	871
	Met Lys Leu Ser Glu Glu Asn Arg His Leu Arg Asp Glu Gly Leu Arg	
	180 185 190 195	
	ctc aga aag gta gca cat tcg gat aaa cct gga tca acc tca act gca	919
20	Leu Arg Lys Val Ala His Ser Asp Lys Pro Gly Ser Thr Ser Thr Ala	
	200 205 210	
	tcc ttc aga gat aat gtc acc agt cct ctt cct tca ctt ctt gtt gta	967
	Ser Phe Arg Asp Asn Val Thr Ser Pro Leu Pro Ser Leu Leu Val Val	
	215 220 225	
25	att gca gcc att ttc att gga ttc ttt cta ggg aaa ttc atc ttg	1012
	Ile Ala Ala Ile Phe Ile Gly Phe Phe Leu Gly Lys Phe Ile Leu	
	230 235 240	
	tagagtgaag catgcagagt gctgtttctt tttttttttt ttctcttgac cagaaaaa	1070
	gatttggtta cctaccattt cattggtagt atggcccacg gtgaccattt ttttgtgtgt	1130
30	acagcgtcat ataggttttg cctttaatga tctcttacgg ttagaaaaca caataaaaac	1190
	aaactgttcg gctactggac aggttgata ttaccagatc atcactagca gatgtcagtt	1250
	gcacattgag tcctttatga aattcataaa taaagaattg ttctttcttt gtgggtttta	1310
	taagagttca agaattgttc agagtcttgt aaatgttatt ttaataatcc ctttaaattt	1370
	tatctgttgc tgttacctct tgaaatatga tttatttaga ttgctaatacc cactcattca	1430
35	ggaaatgccca agaggtattc cttggggaaa tgggtgcctct tacagtgtaa atttttctc	1490

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ctttaccttt gctaatatca tggcagaatt tttcttatcc cttgtgaggc agttgttgac 1550
 tgagtttttc atccttaciaa tcctgtccca tgggtatttaa cataaaaaaa aataaaaactg 1610
 ttaacagat 1619

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 10 <221> CDS
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 15 gacc atg ttc gtt ccc tgc ggg gag tgc gcc ccc gac ctt gcc ggc ttc 109
 Met Phe Val Pro Cys Gly Glu Ser Ala Pro Asp Leu Ala Gly Phe
 1 5 10 15
 acc ctc cta atg cca gca gta tct gtt gga aat gtt ggc cag ctt gca 157
 Thr Leu Leu Met Pro Ala Val Ser Val Gly Asn Val Gly Gln Leu Ala
 20 20 25 30
 atg gat ctg att att tct aca ctg aat atg tct aag att ggt tac ttc 205
 Met Asp Leu Ile Ile Ser Thr Leu Asn Met Ser Lys Ile Gly Tyr Phe
 35 40 45
 tat acc gat tgt ctt gtg cca atg gtt gga aac aat cca tat gcg acc 253
 25 Tyr Thr Asp Cys Leu Val Pro Met Val Gly Asn Asn Pro Tyr Ala Thr
 50 55 60
 aca gaa gga aat tca aca gaa ctt agc ata aat gct gaa gtg tat tca 301
 Thr Glu Gly Asn Ser Thr Glu Leu Ser Ile Asn Ala Glu Val Tyr Ser
 65 70 75
 30 ttg cct tca aga aag ctg gtg gct cta cag tta aga tcc att ttt att 349
 Leu Pro Ser Arg Lys Leu Val Ala Leu Gln Leu Arg Ser Ile Phe Ile
 80 85 90 95
 aag tat aaa tca aag cca ttc tgt gaa aaa ctg ctt tcc tgg gtg aaa 397
 Lys Tyr Lys Ser Lys Pro Phe Cys Glu Lys Leu Leu Ser Trp Val Lys
 35 100 105 110

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	agc agt ggc tgt gcc aga gtc att gtt ctt tcg agc agt cat tca tat	445
	Ser Ser Gly Cys Ala Arg Val Ile Val Leu Ser Ser Ser His Ser Tyr	
	115 120 125	
5	cag cgt aat gat ctg cag ctt cgt agt act ccc ttc cgg tac cta ctt	493
	Gln Arg Asn Asp Leu Gln Leu Arg Ser Thr Pro Phe Arg Tyr Leu Leu	
	130 135 140	
	aca cct tcc atg caa aaa agt gtt caa aat aaa ata aag agc ctt aac	541
	Thr Pro Ser Met Gln Lys Ser Val Gln Asn Lys Ile Lys Ser Leu Asn	
	145 150 155	
10	tgg gaa gaa atg gaa aaa agc cgg tgc att cct gaa ata gat gat tcc	589
	Trp Glu Glu Met Glu Lys Ser Arg Cys Ile Pro Glu Ile Asp Asp Ser	
	160 165 170 175	
	gag ttt tgt atc cgc att ccg gga gga ggt atc aca aaa aca ctc tat	637
	Glu Phe Cys Ile Arg Ile Pro Gly Gly Gly Ile Thr Lys Thr Leu Tyr	
15	180 185 190	
	gat gaa agc tgt tct aaa gaa atc caa atg gca gtt ctg ctg aaa ttt	685
	Asp Glu Ser Cys Ser Lys Glu Ile Gln Met Ala Val Leu Leu Lys Phe	
	195 200 205	
20	gtt tca gaa ggg gac aac atc cca gat gca tta ggt ctt gtt gag tat	733
	Val Ser Glu Gly Asp Asn Ile Pro Asp Ala Leu Gly Leu Val Glu Tyr	
	210 215 220	
	ctt aat gag tgg ctt cag ata ctc aaa cca ctt agc gat gac ccc aca	781
	Leu Asn Glu Trp Leu Gln Ile Leu Lys Pro Leu Ser Asp Asp Pro Thr	
	225 230 235	
25	gta tct gcc tca cgg tgg aaa ata cca agt tct tgg aga tta ctc ttt	829
	Val Ser Ala Ser Arg Trp Lys Ile Pro Ser Ser Trp Arg Leu Leu Phe	
	240 245 250 255	
	ggc agt ggt ctt ccc cct gca ctt ttc tgatctaatt tctgttttat acct	880
	Gly Ser Gly Leu Pro Pro Ala Leu Phe	
30	260	
	tatacccaaaa acacttacta ccaacacagc tgtaaacaat tctatacaaaa aaaattgtat	940
	gatctggtat taggaaatta ctttcacagt aaatatcaaaa gaaaaaagat taagggtctc	1000
	tttgccatgc ttttcatcat atgcaccaaaa tgtaaatttt gtacaataaaa attttatttc	1060
	ctaagt	1066

35

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<211> 618

<212> DNA

<213> Homo sapiens

5 <220>

<221> CDS

<222> (54) ... (392)

<400> 25

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Met

1

ggg tct cgg ttg tcc cag cct ttt gag tcc tat atc act gcg cct ccc 104
Gly Ser Arg Leu Ser Gln Pro Phe Glu Ser Tyr Ile Thr Ala Pro Pro

15	5	10	15	
ggt acc gcc gcc gcg ccc gcc aaa cct gcg ccc cca gct aca ccc gga				152
Gly Thr Ala Ala Ala Pro Ala Lys Pro Ala Pro Pro Ala Thr Pro Gly				
	20	25	30	

gcg ccg acc tcc cca gca gaa cac cgc ctg ttg aag acc tgc tgg agc 200
20 Ala Pro Thr Ser Pro Ala Glu His Arg Leu Leu Lys Thr Cys Trp Ser
35 40 45

tgt cgc gtg ctt tct ggg ttg ggg ctg atg ggg gcg ggc ggg tac gtg 248
Cys Arg Val Leu Ser Gly Leu Gly Leu Met Gly Ala Gly Gly Tyr Val
50 55 60 65

25 tac tgg gtg gca cgg aag ccc atg aag atg gga tac ccc ccg agt cca 296
Tyr Trp Val Ala Arg Lys Pro Met Lys Met Gly Tyr Pro Pro Ser Pro
70 75 80

tgg acc att acg cag atg gtc atc ggc ctc agc att gcc acc tgg ggt 344
Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Ile Ala Thr Trp Gly

30	85	90	95	
	atc gtt gtc atg gca gac ccc aaa ggg aag gcc tac cgc gtt gtt t			390
	Ile Val Val Met Ala Asp Pro Lys Gly Lys Ala Tyr Arg Val Val			

100 105 110
gaaagtacca ccagtgaatc tgtcttctgt ctctgtccct ttccccgtga cacacacagc 450

35 aggcattggaa tttaatgggt gttctggaca gacacttgta catggacaga catcactact 510

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gtggatacta caagactgag aagaaaatcg tatgttgtca ttctctggct atggagtgtt 570
 tgtggccttc acagatttca caggaaccaa taaatccctc agagaagt 618

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 15 ggtgagcggg cgctagggcc gcgagccccc gccggccctt cctccagcgc cctgcggacc 180
 ccgcagaagg cgctcgctc cctagcccg caaaaacatat cgatttttct cgctgtggca 240
 acggggacgt cctgatagat cctctgctcc aataggcaac tccggccttc cctgccctga 300
 cctggaacct ctgggagggc tgcagagtaa gtgccgcctc tgcgctccga cggaggcaacg 360
 aggctgtgg agtaggtccc tctgttccga caggtgcgac acttggcgct cc atg ctt 418
 20 Met Leu
 1
 gcg ggt gcc ggg agg cct ggc ctc ccc cag ggc cgc cac ctc tgc tgg 466
 Ala Gly Ala Gly Arg Pro Gly Leu Pro Gln Gly Arg His Leu Cys Trp
 5 10 15
 25 ttg ctc tgt gct ttc acc tta aag ctc tgc caa gca gag gct ccc gtg 514
 Leu Leu Cys Ala Phe Thr Leu Lys Leu Cys Gln Ala Glu Ala Pro Val
 20 25 30
 cag gaa gag aag ctg tca gca agc acc tca aat ttg cca tgc tgg ctg 562
 Gln Glu Glu Lys Leu Ser Ala Ser Thr Ser Asn Leu Pro Cys Trp Leu
 30 35 40 45 50
 gtg gaa gag ttt gtg gta gca gaa gag tgc tct cca tgc tct aat ttc 610
 Val Glu Glu Phe Val Val Ala Glu Glu Cys Ser Pro Cys Ser Asn Phe
 55 60 65
 cgg gct aaa act acc cct gag tgt ggt ccc aca gga tat gta gag aaa 658
 35 Arg Ala Lys Thr Thr Pro Glu Cys Gly Pro Thr Gly Tyr Val Glu Lys

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	70	75	80	
	atc aca tgc agc tca tct aag aga aat gag ttc aaa agc tgc cgc tca			706
	Ile Thr Cys Ser Ser Ser Lys Arg Asn Glu Phe Lys Ser Cys Arg Ser			
	85	90	95	
5	gct ttg atg gaa caa cgc tta ttt tgg aag ttc gaa ggg gct gtc gtg			754
	Ala Leu Met Glu Gln Arg Leu Phe Trp Lys Phe Glu Gly Ala Val Val			
	100	105	110	
	tgt gtg gcc ctg atc ttc gct tgt ctt gtc atc att cgt cag cga caa			802
	Cys Val Ala Leu Ile Phe Ala Cys Leu Val Ile Ile Arg Gln Arg Gln			
10	115	120	125	130
	ttg gac aga aag gct ctg gaa aag gtc cgg aag caa atc gag tcc ata			850
	Leu Asp Arg Lys Ala Leu Glu Lys Val Arg Lys Gln Ile Glu Ser Ile			
	135	140	145	
	tagctacatt ccacccttgt atcctgggtc ttagagaccc tatctcagac agtgaaagtg			910
15	aaatggactg atttgcactc ttggttcttt ggagccttgt ggtggaatcc ccttttcccc			970
	atcttcttct ttcagatcat taatgagcag aataaaaaga gtaaatggt t			1021
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	gcccagatcc gggggcgccc cggtgtcccc tccagagctg ctgcactcca cgcccccta			120
	ccagggtcc agccccagc gaaatctccg accaggcccc cccaggagcc agatccaggc			180
30	tcttggaaga accatgtccg gcagctactg gtcattgccag gcacacactg ctgcccgaaga			240
	ggagctgctg tttgaattat ctgtgaatgt tgggaagagg aatgccagag ctgccggctg			300
	aaaattaccc aaccaagaga aatctgcagg atg gac ttt ctg gtc etc ttc ttg			354
	Met Asp Phe Leu Val Leu Phe Leu			
	1	5		
35	ttc tac ctg gct tcc gtg ctg atg ggt ctt gtt ctt atc tgc gtc tgc			402

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	Phe Tyr Leu Ala Ser Val Leu Met Gly Leu Val Leu Ile Cys Val Cys	
	10 15 20	
	tgc aaa acc cat agc ttg aaa ggc ctg gcc agg gga gga gca cag ata	450
	Ser Lys Thr His Ser Leu Lys Gly Leu Ala Arg Gly Gly Ala Gln Ile	
5	25 30 35 40	
	ttt tcc tgt ata att cca gaa tgt ctt cag aga gcc gtg cat gga ttg	498
	Phe Ser Cys Ile Ile Pro Glu Cys Leu Gln Arg Ala Val His Gly Leu	
	45 50 55	
	ctt cat tac ctt ttc cat acg aga aac cac acc ttc att gtc ctg cac	546
10	Leu His Tyr Leu Phe His Thr Arg Asn His Thr Phe Ile Val Leu His	
	60 65 70	
	ctg gtc ttg caa ggg atg gtt tat act gag tac acc tgg gaa gta ttt	594
	Leu Val Leu Gln Gly Met Val Tyr Thr Glu Tyr Thr Trp Glu Val Phe	
	75 80 85	
15	ggc tac tgt cag gag ctg gag ttg tcc ttg cat tac ctt ctt ctg ccc	642
	Gly Tyr Cys Gln Glu Leu Glu Leu Ser Leu His Tyr Leu Leu Leu Pro	
	90 95 100	
	tat ctg ctg cta ggt gta aac ctg ttt ttt ttc acc ctg act tgt gga	690
	Tyr Leu Leu Leu Gly Val Asn Leu Phe Phe Phe Thr Leu Thr Cys Gly	
20	105 110 115 120	
	acc aat cct ggc att ata aca aaa gca aat gaa tta tta ttt ctt cat	738
	Thr Asn Pro Gly Ile Ile Thr Lys Ala Asn Glu Leu Leu Phe Leu His	
	125 130 135	
	gtt tat gaa ttt gat gaa gtg atg ttt cca aag aac gtg agg tgc tct	786
25	Val Tyr Glu Phe Asp Glu Val Met Phe Pro Lys Asn Val Arg Cys Ser	
	140 145 150	
	act tgt gat tta agg aaa cca gct cga tcc aag cac tgc agt gtg tgt	834
	Thr Cys Asp Leu Arg Lys Pro Ala Arg Ser Lys His Cys Ser Val Cys	
	155 160 165	
30	aac tgg tgt gtg cac cgt ttc gac cat cac tgt gtt tgg gtg aac aac	882
	Asn Trp Cys Val His Arg Phe Asp His His Cys Val Trp Val Asn Asn	
	170 175 180	
	tgc atc ggg gcc tgg aac atc agg tac ttc ctc atc tac gtc ttg acc	930
	Cys Ile Gly Ala Trp Asn Ile Arg Tyr Phe Leu Ile Tyr Val Leu Thr	
35	185 190 195 200	

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	ttg acg gcc tcg gct gcc acc gtc gcc att gtg agc acc act ttt ctg	978
	Leu Thr Ala Ser Ala Ala Thr Val Ala Ile Val Ser Thr Thr Phe Leu	
	205 210 215	
5	gtc cac ttg gtg gtg atg tca gat tta tac cag gag act tac atc gat	1026
	Val His Leu Val Val Met Ser Asp Leu Tyr Gln Glu Thr Tyr Ile Asp	
	220 225 230	
	gac ctt gga cac ctc cat gtt atg gac acg gtc ttt ctt att cag tac	1074
	Asp Leu Gly His Leu His Val Met Asp Thr Val Phe Leu Ile Gln Tyr	
	235 240 245	
10	ctg ttc ctg act ttt cca cgg att gtc ttc atg ctg ggc ttt gtc gtg	1122
	Leu Phe Leu Thr Phe Pro Arg Ile Val Phe Met Leu Gly Phe Val Val	
	250 255 260	
	GTT CTG AGC TTC CTC CTG GGT GGC TAC CTG TTG TTT GTC CTG TAT CTG	1170
	Val Leu Ser Phe Leu Leu Gly Gly Tyr Leu Leu Phe Val Leu Tyr Leu	
15	265 270 275 280	
	gcg gcc acc aac cag act act aac gag tgg tac aga ggt gac tgg gcc	1218
	Ala Ala Thr Asn Gln Thr Thr Asn Glu Trp Tyr Arg Gly Asp Trp Ala	
	285 290 295	
20	tgg tgc cag cgt tgt ccc ctt gtg gcc tgg cct ccg tca gca gag ccc	1266
	Trp Cys Gln Arg Cys Pro Leu Val Ala Trp Pro Pro Ser Ala Glu Pro	
	300 305 310	
	caa gtc cac cgg aac att cac tcc cat ggg ctt cgg agc aac ctt caa	1314
	Gln Val His Arg Asn Ile His Ser His Gly Leu Arg Ser Asn Leu Gln	
	315 320 325	
25	gag atc ttt cta cct gcc ttt cca tgt cat gag agg aag aaa caa gaa	1362
	Glu Ile Phe Leu Pro Ala Phe Pro Cys His Glu Arg Lys Lys Gln Glu	
	330 335 340	
	tgacaagtgt atgactgcct ttgagctgta gttcccgttt atttacacat gtggatcc	1420
30	tcgtttttcca ag	1432
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	<213> Homo sapiens	
35	<220>	

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<221> CDS

<222> (62)...(355)

<400> 28

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	Met Thr Lys Lys Lys Arg Glu Asn Leu Gly Val Ala Leu Glu Ile Asp	
	1 5 10 15	
	ggg cta gag gag aag ctg tcc cag tgt cgg aga gac ctg gag gcc gtg	157
10	Gly Leu Glu Glu Lys Leu Ser Gln Cys Arg Arg Asp Leu Glu Ala Val	
	20 25 30	
	aac tcc aga ctc cac agc cgg gag ctg agc cca gag gcc agg agg tcc	205
	Asn Ser Arg Leu His Ser Arg Glu Leu Ser Pro Glu Ala Arg Arg Ser	
	35 40 45	
15	ctg gag aag gag aaa aac agc cta atg aac aaa gcc tcc aac tac gag	253
	Leu Glu Lys Glu Lys Asn Ser Leu Met Asn Lys Ala Ser Asn Tyr Glu	
	50 55 60	
	aag gaa ctg aag ttt ctt cgg caa gag aac cgg aag aac atg ctg ctc	301
	Lys Glu Leu Lys Phe Leu Arg Gln Glu Asn Arg Lys Asn Met Leu Leu	
20	65 70 75 80	
	tct gtg gcc atc ttt atc ctc ctg acg ctc gtc tat gcc tac tgg acc	349
	Ser Val Ala Ile Phe Ile Leu Leu Thr Leu Val Tyr Ala Tyr Trp Thr	
	85 90 95	
	atg tgagcctggc acttccccac aaccagcaca ggcttccact tggcccct	400
25	Met	
	tgatcaggat caagcaggca cttcaagcct caataggacc aaggtgctgg ggtgttcccc	460
	tcccaacctg gtgttcaagc atggcttccct ggcgccccag gccttgccctc cctggcctgc	520
	tgggggggttc cgggtctcca gaaggacatg gtgctggtcc ctcccttagc ccaagggaga	580
30	ggcaataaag acacaaagct g	601

<210> 29

<211> 585

<212> DNA

35 <213> Homo sapiens

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<220>

<221> CDS

<222> (78)...(452)

5 <400> 29
 actaacctct gccctgcagc cgcgagggcg cgcgggaaat cccgagtgc tctggaatac 60
 gcagagtcag taagacc atg gct acg tcc tcg atg tct aag ggt tgc ttt 110
 Met Ala Thr Ser Ser Met Ser Lys Gly Cys Phe
 1 5 10
 10 gtt ttt aag cca aac tcc aaa aag aga aag atc tct ctg cca ata gag 158
 Val Phe Lys Pro Asn Ser Lys Lys Arg Lys Ile Ser Leu Pro Ile Glu
 15 15 20 25
 gac tat ttt aac aaa ggg aaa aat gag cct gag gac agt aag ctt cga 206
 Asp Tyr Phe Asn Lys Gly Lys Asn Glu Pro Glu Asp Ser Lys Leu Arg
 15 30 35 40
 ttc gaa act tat cag ttg ata tgg cag cag atg aaa tct gaa aat gag 254
 Phe Glu Thr Tyr Gln Leu Ile Trp Gln Gln Met Lys Ser Glu Asn Glu
 45 50 55
 cga cta caa gag gaa tta aat aaa aac ttg ttt gac aat ctg att gaa 302
 20 Arg Leu Gln Glu Glu Leu Asn Lys Asn Leu Phe Asp Asn Leu Ile Glu
 60 65 70 75
 ttt ctg caa aaa tca cat tct gga ttc cag aag aat tca aga gac ttg 350
 Phe Leu Gln Lys Ser His Ser Gly Phe Gln Lys Asn Ser Arg Asp Leu
 80 85 90
 25 ggc ggt caa ata aaa ctc aga gaa att cca act gct gct ctt gtt ctt 398
 Gly Gly Gln Ile Lys Leu Arg Glu Ile Pro Thr Ala Ala Leu Val Leu
 95 100 105
 ggt ata tat gcg tat gtt tgt tca tgc atg cat ctc tgt gta ttt cgt 446
 Gly Ile Tyr Ala Tyr Val Cys Ser Cys Met His Leu Cys Val Phe Arg
 110 115 120
 30 ttt taaatttttt tttattgttg agaatagtgg aaggacctgt tttgatgagc c 500
 Phe
 tattttgtct ctcttatttg tacaattaaa ccaactatag tttatattac atattttcaa 560
 35 aaaccaataa aaattcctta tcttt 585

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<210> 30
 <211> 1100
 <212> DNA
 5 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (57)...(1040)

10 <400> 30
 agaccgacct tgaccgccca cctggcagga gcaggacagg acggccggac gcggcc atg 59
 Met
 1
 gcc gag ctc ccg ggg ccc ttt ctc tgc ggg gcc ctg cta ggc ttc ctg 107
 15 Ala Glu Leu Pro Gly Pro Phe Leu Cys Gly Ala Leu Leu Gly Phe Leu
 5 10 15
 tgc ctg agt ggg ctg gcc gtg gag gtg aag gta ccc aca gag ccg ctg 155
 Cys Leu Ser Gly Leu Ala Val Glu Val Lys Val Pro Thr Glu Pro Leu
 20 25 30
 20 agc acg ccc ctg ggg aag aca gcc gag ctg acc tgc acc tac agc acg 203
 Ser Thr Pro Leu Gly Lys Thr Ala Glu Leu Thr Cys Thr Tyr Ser Thr
 35 40 45
 tcg gtg gga gac agc ttc gcc ctg gag tgg agc ttt gtg cag cct ggg 251
 Ser Val Gly Asp Ser Phe Ala Leu Glu Trp Ser Phe Val Gln Pro Gly
 25 50 55 60 65
 aaa ccc atc tct gag tcc cat cca atc ctg tac ttc acc aat ggc cat 299
 Lys Pro Ile Ser Glu Ser His Pro Ile Leu Tyr Phe Thr Asn Gly His
 70 75 80
 ctg tat cca act ggt tct aag tca aag cgg gtc agc ctg ctt cag aac 347
 30 Leu Tyr Pro Thr Gly Ser Lys Ser Lys Arg Val Ser Leu Leu Gln Asn
 85 90 95
 ccc ccc aca gtg ggg gtg gcc aca ctg aaa ctg act gac gtc cac ccc 395
 Pro Pro Thr Val Gly Val Ala Thr Leu Lys Leu Thr Asp Val His Pro
 100 105 110
 35 tca gat act gga acc tac ctc tgc caa gtc aac aac cca cca gat ttc 443

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	Ser Asp Thr Gly Thr Tyr Leu Cys Gln Val Asn Asn Pro Pro Asp Phe			
	115	120	125	
	tac acc aat ggg ttg ggg cta atc aac ctt act gtg ctg gtt ccc ccc		491	
	Tyr Thr Asn Gly Leu Gly Leu Ile Asn Leu Thr Val Leu Val Pro Pro			
5	130	135	140	145
	agt aat ccc tta tgc agt cag agt gga caa acc tct gtg gga ggc tct			539
	Ser Asn Pro Leu Cys Ser Gln Ser Gly Gln Thr Ser Val Gly Gly Ser			
	150	155	160	
	act gca ctg aga tgc agc tct tcc gag ggg gct cct aag cca gtg tac			587
10	Thr Ala Leu Arg Cys Ser Ser Ser Glu Gly Ala Pro Lys Pro Val Tyr			
	165	170	175	
	aac tgg gtg cgt ctt gga act ttt cct aca cct tct cct ggc agc atg			635
	Asn Trp Val Arg Leu Gly Thr Phe Pro Thr Pro Ser Pro Gly Ser Met			
	180	185	190	
15	gtt caa gat gag gtg tct ggc cag ctc att ctc acc aac ctc tcc ctg			683
	Val Gln Asp Glu Val Ser Gly Gln Leu Ile Leu Thr Asn Leu Ser Leu			
	195	200	205	
	acc tcc tcg ggc acc tac cgc tgt gtg gcc acc aac cag atg ggc agt			731
	Thr Ser Ser Gly Thr Tyr Arg Cys Val Ala Thr Asn Gln Met Gly Ser			
20	210	215	220	225
	gca tcc tgt gag ctg acc ctc tct gtg acc gaa ccc tcc caa ggc cga			779
	Ala Ser Cys Glu Leu Thr Leu Ser Val Thr Glu Pro Ser Gln Gly Arg			
	230	235	240	
	gtg gcc gga gct ctg att ggg gtg ctc ctg ggc gtg ctg ttg ctg tca			827
25	Val Ala Gly Ala Leu Ile Gly Val Leu Leu Gly Val Leu Leu Leu Ser			
	245	250	255	
	gtt gct gcg ttc tgc ctg gtc agg ttc cag aaa gag agg ggg aag aag			875
	Val Ala Ala Phe Cys Leu Val Arg Phe Gln Lys Glu Arg Gly Lys Lys			
	260	265	270	
30	ccc aag gag aca tat ggg ggt agt gac ctt cgg gag gat gcc atc gct			923
	Pro Lys Glu Thr Tyr Gly Gly Ser Asp Leu Arg Glu Asp Ala Ile Ala			
	275	280	285	
	cct ggg atc tct gag cac act tgt atg agg gct gat tct agc aag ggg			971
	Pro Gly Ile Ser Glu His Thr Cys Met Arg Ala Asp Ser Ser Lys Gly			
35	290	295	300	305

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ttc ctg gaa aga ccc tcg tct gcc agc acc gtg acg acc acc aag tcc 1019

Phe Leu Glu Arg Pro Ser Ser Ala Ser Thr Val Thr Thr Thr Lys Ser

310

315

320

aag ctc cct atg gtc gtg tgacttctcc cgatccctga gggcgggtgag ggg 1070

5 Lys Leu Pro Met Val Val

325

gaatatcaat aattaaagtc tgtgggtacc 1100

<210> 31

10 <211> 313

<212> PRT

<213> Homo sapiens

<400> 31

15 Met Asn Gln Leu Ser Phe Leu Leu Phe Leu Ile Ala Thr Thr Arg Gly

1

5

10

15

Trp Ser Thr Asp Glu Ala Asn Thr Tyr Phe Lys Glu Trp Thr Cys Ser

20

25

30

Ser Ser Pro Ser Leu Pro Arg Ser Cys Lys Glu Ile Lys Asp Glu Cys

20

35

40

45

Pro Ser Ala Phe Asp Gly Leu Tyr Phe Leu Arg Thr Glu Asn Gly Val

50

55

60

Ile Tyr Gln Thr Phe Cys Asp Met Thr Ser Gly Gly Gly Gly Trp Thr

65

70

75

80

25 Leu Val Ala Ser Val His Glu Asn Asp Met Arg Gly Lys Cys Thr Val

85

90

95

Gly Asp Arg Trp Ser Ser Gln Gln Gly Ser Lys Ala Asp Tyr Pro Glu

100

105

110

Gly Asp Gly Asn Trp Ala Asn Tyr Asn Thr Phe Gly Ser Ala Glu Ala

30

115

120

125

Ala Thr Ser Asp Asp Tyr Lys Asn Pro Gly Tyr Tyr Asp Ile Gln Ala

130

135

140

Lys Asp Leu Gly Ile Trp His Val Pro Asn Lys Ser Pro Met Gln His

145

150

155

160

35 Trp Arg Asn Ser Ser Leu Leu Arg Tyr Arg Thr Asp Thr Gly Phe Leu

32/177

165 170 175
 Gln Thr Leu Gly His Asn Leu Phe Gly Ile Tyr Gln Lys Tyr Pro Val
 180 185 190
 Lys Tyr Gly Glu Gly Lys Cys Trp Thr Asp Asn Gly Pro Val Ile Pro
 5 195 200 205
 Val Val Tyr Asp Phe Gly Asp Ala Gln Lys Thr Ala Ser Tyr Tyr Ser
 210 215 220
 Pro Tyr Gly Gln Arg Glu Phe Thr Ala Gly Phe Val Gln Phe Arg Val
 225 230 235 240
 10 Phe Asn Asn Glu Arg Ala Ala Asn Ala Leu Cys Ala Gly Met Arg Val
 245 250 255
 Thr Gly Cys Asn Thr Glu His His Cys Ile Gly Gly Gly Tyr Phe
 260 265 270
 Pro Glu Ala Ser Pro Gln Gln Cys Gly Asp Phe Ser Gly Phe Asp Trp
 15 275 280 285
 Ser Gly Tyr Gly Thr His Val Gly Tyr Ser Ser Ser Arg Glu Ile Thr
 290 295 300
 Glu Ala Ala Val Leu Leu Phe Tyr Arg
 305 310
 20
 <210> 32
 <211> 229
 <212> PRT
 <213> Homo sapiens
 25
 <400> 32
 Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
 1 5 10 15
 Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
 30 20 25 30
 Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
 35 40 45
 Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
 50 55 60
 35 Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu

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65 70 75 80
 Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
 85 90 95
 Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
 5 100 105 110
 Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
 115 120 125
 Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
 130 135 140
 10 Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile
 145 150 155 160
 Asn Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu
 165 170 175
 Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe
 15 180 185 190
 Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val
 195 200 205
 Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys
 210 215 220
 20 Arg Lys Ser Arg Thr
 225

 <210> 33
 <211> 467
 25 <212> PRT
 <213> Homo sapiens

 <400> 33
 Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
 30 1 5 10 15
 Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
 20 25 30
 Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
 35 40 45
 35 Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe

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	50	55	60
	Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys		
	65	70	75 80
5	Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro	85	90 95
	Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe	100	105 110
	Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr	115	120 125
10	Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser	130	135 140
	Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp	145	150 155 160
	Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg	165	170 175
15	Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu	180	185 190
	Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys	195	200 205
20	Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val	210	215 220
	Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser	225	230 235 240
	Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr	245	250 255
25	Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly	260	265 270
	Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro	275	280 285
30	His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr	290	295 300
	Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val	305	310 315 320
	Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn	325	330 335
35			

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Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
 340 345 350
 Leu Arg Gln Met Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
 355 360 365
 5 Glu Thr His Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
 370 375 380
 Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
 385 390 395 400
 Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
 10 405 410 415
 Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
 420 425 430
 Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
 435 440 445
 15 Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
 450 455 460
 Asn Val Ile
 465
 20 <210> 34
 <211> 99
 <212> PRT
 <213> Homo sapiens
 25 <400> 34
 Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser
 1 5 10 15
 Val Lys Gly His Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu
 20 25 30
 30 Val Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro
 35 40 45
 Glu Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr
 50 55 60
 Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu
 35 65 70 75 80

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Phe Asn Pro Ser Gly Pro Tyr Gln Gln Lys Pro Val His Glu Lys Lys
 85 90 95

Glu Val Leu

5 <210> 35
 <211> 189
 <212> PRT
 <213> Homo sapiens

10 <400> 35
 Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
 1 5 10 15
 Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val
 20 25 30
 15 Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu
 35 40 45
 Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys
 50 55 60
 Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln
 20 65 70 75 80
 Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu
 85 90 95
 Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala
 100 105 110
 25 Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly
 115 120 125
 Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg
 130 135 140
 Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr
 30 145 150 155 160
 His Gly Leu Ser Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly
 165 170 175
 Leu Cys Leu Ala Gly Leu Ala Leu Glu Ile Arg Ser Leu
 180 185

35

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<210> 36

<211> 363

<212> PRT

<213> Homo sapiens

5

<400> 36

Met Val Asp Ser Leu Leu Ala Val Thr Leu Ala Gly Asn Leu Gly Leu
 1 5 10 15
 Thr Phe Leu Arg Gly Ser Gln Thr Gln Ser His Pro Asp Leu Gly Thr
 10 20 25 30
 Glu Gly Cys Trp Asp Gln Leu Ser Ala Pro Arg Thr Phe Thr Leu Leu
 35 40 45
 Asp Pro Lys Ala Ser Leu Leu Thr Lys Ala Phe Leu Asn Gly Ala Leu
 50 55 60
 15 Asp Gly Val Ile Leu Gly Asp Tyr Leu Ser Arg Thr Pro Glu Pro Arg
 65 70 75 80
 Pro Ser Leu Ser His Leu Leu Ser Gln Tyr Tyr Gly Ala Gly Val Ala
 85 90 95
 Arg Asp Pro Gly Phe Arg Ser Asn Phe Arg Arg Gln Asn Gly Ala Ala
 100 105 110
 20 Leu Thr Ser Ala Ser Ile Leu Ala Gln Gln Val Trp Gly Thr Leu Val
 115 120 125
 Leu Leu Gln Arg Leu Glu Pro Val His Leu Gln Leu Gln Cys Met Ser
 130 135 140
 25 Gln Glu Gln Leu Ala Gln Val Ala Ala Asn Ala Thr Lys Glu Phe Thr
 145 150 155 160
 Glu Ala Phe Leu Gly Cys Pro Ala Ile His Pro Arg Cys Arg Trp Gly
 165 170 175
 Ala Ala Pro Tyr Arg Gly Arg Pro Lys Leu Leu Gln Leu Pro Leu Gly
 180 185 190
 30 Phe Leu Tyr Val His His Thr Tyr Val Pro Ala Pro Pro Cys Thr Asp
 195 200 205
 Phe Thr Arg Cys Ala Ala Asn Met Arg Ser Met Gln Arg Tyr His Gln
 210 215 220
 35 Asp Thr Gln Gly Trp Gly Asp Ile Gly Tyr Ser Phe Val Val Gly Ser

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225 230 235 240
 Asp Gly Tyr Val Tyr Glu Gly Arg Gly Trp His Trp Val Gly Ala His
 245 250 255
 Thr Leu Gly His Asn Ser Arg Gly Phe Gly Val Ala Ile Val Gly Asn
 5 260 265 270
 Tyr Thr Ala Ala Leu Pro Thr Glu Ala Ala Leu Arg Thr Val Arg Asp
 275 280 285
 Thr Leu Pro Ser Cys Ala Val Arg Ala Gly Leu Leu Arg Pro Asp Tyr
 290 295 300
 10 Ala Leu Leu Gly His Arg Gln Leu Val Arg Thr Asp Cys Pro Gly Asp
 305 310 315 320
 Ala Leu Phe Asp Leu Leu Arg Thr Trp Pro His Phe Thr Ala Thr Val
 325 330 335
 Lys Pro Arg Pro Ala Arg Ser Val Ser Lys Arg Ser Arg Arg Glu Pro
 15 340 345 350
 Pro Pro Arg Thr Leu Pro Ala Thr Asp Leu Gln
 355 360

 <210> 37
 20 <211> 249
 <212> PRT
 <213> Homo sapiens

 <400> 37
 25 Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu
 1 5 10 15
 Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg
 20 25 30
 Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Glu Asp
 30 35 40 45
 Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu Gln Leu Gln
 50 55 60
 Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val Ile Ile Glu
 65 70 75 80
 35 Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser Val Asn Gln

39/177

	85	90	95
	Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala Asn Lys Ile		
	100	105	110
5	Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn Ala Leu Asn		
	115	120	125
	Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys Val Gln Val		
	130	135	140
	Leu Lys Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly		
	145	150	155
10	Leu Leu Arg Ala Gln Val Asp Ser Ser Phe Leu Ser Leu Tyr Asp Ser		
	165	170	175
	His Val Ala Lys Glu Ile Leu Leu Arg Val Leu Thr Leu Phe Gln Asn		
	180	185	190
	Ile Lys Asn Cys Leu Lys Ile Glu Gly His Leu Ala Val Gln Pro Thr		
15	195	200	205
	Phe Thr Glu Gly Ser Leu Phe Phe Leu Leu His Gly Glu Glu Cys Ala		
	210	215	220
	Gln Lys Ile Arg Ala Leu Val Asp His His Asp Ala Glu Val Lys Glu		
	225	230	235
20	Lys Val Val Thr Ile Ile Pro Lys Ile		
	245		
	<210> 38		
	<211> 98		
25	<212> PRT		
	<213> Homo sapiens		
	<400> 38		
	Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile		
30	1	5	10
	Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe		
	20	25	30
	Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu		
	35	40	45
35	Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu Gln		

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50 55 60
 Val Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Leu Gly
 65 70 75 80
 Gly Phe Ser Phe Cys Gln Val Arg Leu Asn Lys Arg Lys Glu Tyr Met
 5 85 90 95
 Val Arg

 <210> 39
 <211> 172
 10 <212> PRT
 <213> Homo sapiens

 <400> 39
 Met Val Gly Pro Ala Pro Arg Arg Arg Leu Arg Pro Leu Ala Ala Leu
 15 1 5 10 15
 Ala Leu Val Leu Ala Leu Ala Pro Gly Leu Pro Thr Ala Arg Ala Gly
 20 20 25 30
 Gln Thr Pro Arg Pro Ala Glu Arg Gly Pro Pro Val Arg Leu Phe Thr
 35 40 45
 20 Glu Glu Glu Leu Ala Arg Tyr Gly Gly Glu Glu Glu Asp Gln Pro Ile
 50 55 60
 Tyr Leu Ala Val Lys Gly Val Val Phe Asp Val Thr Ser Gly Lys Glu
 65 70 75 80
 Phe Tyr Gly Arg Gly Ala Pro Tyr Asn Ala Leu Thr Gly Lys Asp Ser
 25 85 90 95
 Thr Arg Gly Val Ala Lys Met Ser Leu Asp Pro Ala Asp Leu Thr His
 100 105 110
 Asp Thr Thr Gly Leu Thr Ala Lys Glu Leu Glu Ala Leu Asp Glu Val
 115 120 125
 30 Phe Thr Lys Val Tyr Lys Ala Lys Tyr Pro Ile Val Gly Tyr Thr Ala
 130 135 140
 Arg Arg Ile Leu Asn Glu Asp Gly Ser Pro Asn Leu Asp Phe Lys Pro
 145 150 155 160
 Glu Asp Gln Pro His Phe Asp Ile Lys Asp Glu Phe
 35 165 170

41/177

<210> 40

<211> 120

<212> PRT

5 <213> Homo sapiens

<400> 40

Met Met Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser Ser Lys
 1 5 10 15
 10 Val Lys Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile Asp Leu
 20 25 30
 Gln Phe Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile Ala Leu
 35 40 45
 Ala Thr Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile Gly Ser
 15 50 55 60
 Leu Leu Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg Ala Val
 65 70 75 80
 Pro Val Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe Tyr His
 85 90 95
 20 Leu Arg Ile Ala Tyr Tyr Ala Ser Lys Gly Tyr Arg Gly Tyr Ser Tyr
 100 105 110
 Asp Asp Ile Pro Asp Phe Asp Asp
 115 120

25 <210> 41

<211> 939

<212> DNA

<213> Homo sapiens

30 <400> 41

atgaaccaac tcagcttcct gctgtttctc atagcgacca ccagaggatg gagtacagat 60
 gaggctaata cttacttcaa ggaatggacc tgttcttcgt ctccatctct gccagaagc 120
 tgcaaggaaa tcaaagacga atgtcctagt gcatttgatg gcctgtatct tctccgcact 180
 gagaatggtg ttatctacca gaccttctgt gacatgacct ctgggggtgg cggctggacc 240
 35 ctggtggcca gcgtgcatga gaatgacatg cgtgggaagt gcacgggtgg cgatcgctgg 300

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tccagtcagc agggcagcaa agcagactac ccagaggggg acggcaactg ggccaactac 360
 aacacctttg gatctgcaga ggcggccacg agcgatgact acaagaaccc tggtactac 420
 gacatccagg ccaaggacct gggcatctgg cactgcccc ataagtcccc catgcagcac 480
 tggagaaaca gctccctgct gaggtaccgc acggacactg gcttctcca gacactggga 540
 5 cataatctgt ttggcatcta ccagaaatat ccagtgaat atggagaagg aaagtgttg 600
 actgacaacg gcccggtgat ccctgtggtc tatgattttg gcgacgcca gaaaacagca 660
 tcttattact caccctatgg ccagcgggaa ttcactgagg gatttgttca gttcagggtta 720
 ttaataacg agagagcagc caacgccttg tgtgctggaa tgagggtcac cggatgtaac 780
 actgagcacc actgcattgg tggaggagga tactttccag aggcagtc ccagcagtgt 840
 10 ggagattttt ctggttttga ttggagtggga tatggaactc atgttggtta cagcagcagc 900
 cgtgagataa ctgaggcagc tgtgcttcta ttctatcgt 939

<210> 42

<211> 687

15 <212> DNA

<213> Homo sapiens

<400> 42

atgggcgaca agatctggct gcccttcccc gtgtccttc tggccgctct gcctccggtg 60
 20 ctgctgectg gggcgcccg cttcacacct tcctcgata gcgaactcac ctttaccctt 120
 cccgcgggcc agaaggagt cttctaccag cccatgcccc tgaaggcctc gctggagatc 180
 gagtaccaag ttttagatgg agcaggatta gatattgatt tccatcttgc ctctccagaa 240
 ggcaaaacct tagtttttga acaagaaaa tcagatggag ttcacactgt agagactgaa 300
 gttggtgatt acatgttctg ctttgacaat acattcagca ccatttctga gaagggtgatt 360
 25 ttctttgaat taatcctgga taatatggga gaacaggcac aagaacaaga agattggaag 420
 aaatatatta ctggcacaga tatattggat atgaaactgg aagacatcct ggaatccatc 480
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 gaagetctg atcgaaacat acaagaaagc aactttgata gagtcaattt ctggtctatg 600
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 30 tttgaagata agaggaaaag tagaact 687

<210> 43

<211> 1401

<212> DNA

35 <213> Homo sapiens

43/177

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5	ctggacgccc gccagctgce cgctgggtt gaccaggcca agttcggcat cttcatccac	180
	tggggagtgt tttccgtgcc cagcttcggg agcgagtggg tctgggtgga ttggcaaaag	240
	gaaaagatac cgaagtatgt ggaatttatg aaagataatt accctcctag tttcaaatat	300
	gaagattttg gaccactatt tacagcaaaa ttttttaatg ccaaccagtg ggcagatatt	360
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10	ttgtgggggt cagaatattc gtggaactgg aatgccatag atgagggggc caagagggac	480
	attgtcaagg aacttgaggg agccattagg aacagaactg acctgcgttt tggactgtac	540
	tattcccttt ttgaatggtt tcatccgctc ttcttgagg atgaatccag ttcattccat	600
	aagcggcaat ttccagtttc taagacattg ccagagctct atgagttagt gaacaactat	660
	cagcctgagg ttctgtgggc ggatggtgac ggaggagcac cggatcaata ctggaacagc	720
15	acaggcttct tggcctgggt atataatgaa agcccagttc ggggcacagt agtcaccaat	780
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	tataaccag gacatcttt gccacataaa tgggaaaact gcatgacaat agacaaactg	900
	tcctggggct ataggaggga agctggaatc tctgactatc ttacaattga agaattggtg	960
	aagcaacttg tagagacagt ttcattgtga ggaaatcttt tgatgaatat tgggccca	1020
20	ctagatggca ccatttctgt agtttttgag gacgactga ggcaaatggg gtccctggcta	1080
	aaagtcaatg gagaagctat ttatgaaacc catacctggc gatcccagaa tgacactgtc	1140
	acccagatg tgtggtacac atccaagcct aaagaaaaat tagtctatgc catttttctt	1200
	aatggccca catcaggaca gctgttctt ggccatccca aagetattct gggggcaaca	1260
	gaggtgaaac tactgggcca tggacagcca cttaactgga tttctttgga gcaaaatggc	1320
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	ctagccctga ctaatgtgat c	1401
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	<211> 297	
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	<213> Homo sapiens	
	<400> 44	
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35	gtgaagatgc tgccgctgga tattatcaac tcaactggtaa caacagtatt catgtcctc	120

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gtatctgtgt tggcactgat accagaaacc acaacattga cagttggtgg aggggtgttt 180
gcacttgtga cagcagtatg ctgtcttgcc gacggggccc ttatttaccg gaagcttctg 240
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<211> 567
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10 <400> 45
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cttccccgac ataccttcgg actagtgcag agcaaactct tccccctcta cttccacatc 180
tccatgggct gtgccttcat caacctctgc atcttggtt cacagcatgc ttgggctcag 240
15 ctcacattct gggaggccag ccagctttac ctgctgttcc tgagccttac gctggccact 300
gtcaacgccc gctggetgga accccgcacc acagctgcca tgtgggccct gcaaaccgtg 360
gagaaggagc gaggcctggg tggggaggtta ccaggcagcc accagggtcc cgatccctac 420
cgccagctgc gagagaagga cccaagtac agtgcctctc gccagaattt cttccgctac 480
catgggctgt cctctctttg caatctgggc tgcgtcctga gcaatgggct ctgtctcgt 540
20 ggccttgccc tggaaataag gacctc 567

<210> 46

<211> 1089

<212> DNA

25 <213> Homo sapiens

<400> 46
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ggttcccaga ccagagcca tccagacctg ggaactgagg gctgctggga ccagctctct 120
30 gccctcgga cctttacgct tttggacccc aaggcatctc tgttaaccaa ggccttctc 180
aatggcgccc tggatggggt catccttgga gactacctga gccggactcc tgagccccgg 240
ccatccctca gccacttgct gagccagtac tatggggctg gggtgccag agaccaggg 300
ttccgcagca acttccgacg gcagaacggt gctgctctga cttcagcctc catcctggcc 360
cagcaggtgt ggggaacctt tgctcttcta cagaggctgg agccagtaca cctccagctt 420
35 cagtgcctga gccaaagaaca gctggcccag gtggctgcca atgetaccaa ggaattcact 480

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	gaggcettcc tgggatgccc ggccatccac ccccgtgcc gctggggagc ggcgccttat	540
	cggggccgcc cgaagetgct gcagetgccg ctgggattct tgtacgtgca tcacacctac	600
	gtgcctgcac caccctgcac ggacttcacg cgtgcgcag ccaacatgcg ctccatgcag	660
	cgtaccacc aggacacgca aggetgggga gacatcgget acagtttcgt ggtgggctcg	720
5	gacggctacg tgtacgaggg acgcggctgg cactgggtgg gcgcccacac gctcgggcac	780
	aactcccggg gcttcggcgt ggccatagtg ggcaactaca ccgcggcgt gccaccgag	840
	gccgctctgc gcacggtgcg cgacacgctc ccgagttgtg cgggtgcgcg cggcctcctg	900
	cggccagact acgcgtgct gggccaccgc cagctggtgc gcaccgactg ccccggcgac	960
	gcgtcttcg acctgctgcg cacctggccg cacttcaccg cgactgttaa gccaaacct	1020
10	gccaggagtg tctctaagag atccaggagg gagccacccc caaggaccct gccagccaca	1080
	gacctccaa	1089
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	<211> 747	
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	<213> Homo sapiens	
	<400> 47	
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20	tgctactgca ttacagget gaccgggggt cggcggcggg gcgaccgcga gctcgggata	120
	cgtcttcga agtcgcgaga agacttaact gatggttcat atgatgatgt tctaaatgct	180
	gaacaacttc agaaactcct ttacctgctg gagtcaacgg aggatcctgt aattattgaa	240
	agagctttga ttactttggg taacaatgca gccttttcag ttaaccaagc tattattcgt	300
	gaattgggtg gtattccaat tgttgcaaac aaaatcaacc attccaacca gagtattaaa	360
25	gagaaagctt taaatgcact aaataacctg agtgtgaatg ttgaaaatca aatcaagata	420
	aagggtgcaag ttttgaaact gcttttgaat ttgtctgaaa atccagccat gacagaagga	480
	cttctccgtg cccaagtgga ttcattcttc ctttcccttt atgacagcca cgtagcaaag	540
	gagattcttc ttogagtact tacgctattt cagaatataa agaactgcct caaaatagaa	600
	ggccatttag ctgtgcagcc tactttcact gaaggttcat tgtttttcct gttacatgga	660
30	gaagaatgtg ccagaaaaat aagagcttta gttgatcacc atgatgcaga ggtgaaggaa	720
	aaggttgtaa caataatacc caaaatc	747
	<210> 48	
	<211> 294	
35	<212> DNA	

46/177

<213> Homo sapiens

<400> 48

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tggggagtga tcatgttgat aatgctcgga atatttttca atgtccattc cgctgtgttg 120
attgaggacg ttcccttcac ggagaaagat tttgagaatg gccccagaa catatacaac 180
ctttacgagc aagtcagcta caactgtttc atgctgcag gcctttacct cctcctcgga 240
ggcttctctt tctgccaagt tcggctcaat aagcgcaagg aatacatggt gcgc 294

10 <210> 49

<211> 516

<212> DNA

<213> Homo sapiens

15 <400> 49

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gcgctggccc cggggctgcc cacagcccgg gccgggcaga caccgcgcc tgccgagcgg 120
gggccccag tgcggctttt caccgaggag gagctggccc gctatggcgg ggaggaggaa 180
gatcagccca tctacttggc agtgaaggga gtggtgtttg atgtcacctc cggaaaggag 240
20 ttttatggac gaggagcccc ctacaatgcc ttgacgggga aggactccac tagaggggta 300
gccaatatgt ccttgatcc tgcagacctc acccatgaca ctacgggtct cagggccaag 360
gaactggagg ccctggatga ggtcttcacc aaagtgtaca aagccaaata ccccatcgtc 420
ggctacactg ccgggagaat tctcaatgag gatggcagcc ctaacctgga cttcaagcct 480
gaagaccagc cccattttga catcaaggat gagtgc 516

25

<210> 50

<211> 360

<212> DNA

<213> Homo sapiens

30

<400> 50

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aggtcttcca gcacagacga tggctacatt gaccttcagt ttaagaaaac cctcctaag 120
atcccttata aggcacgc acttgccact gtgctgtttt tgattggcgc ctttctcatt 180
35 attataggct cctcctgct gtcaggctac atcagcaaag ggggggcaga ccgggcgtt 240

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ccagtgetga tcattggcat tctggtgttc ctaccggat tttaccacct gegcateget 300
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<210> 51

5 <211> 1065

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

10 <222> (2)...(943)

<400> 51

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Met Asn Gln Leu Ser Phe Leu Leu Phe Leu Ile Ala Thr Thr Arg Gly

15 1 5 10 15
tgg agt aca gat gag gct aat act tac ttc aag gaa tgg acc tgt tct 97
Trp Ser Thr Asp Glu Ala Asn Thr Tyr Phe Lys Glu Trp Thr Cys Ser

20 20 25 30
tcg tct cca tct ctg ccc aga agc tgc aag gaa atc aaa gac gaa tgt 145
Ser Ser Pro Ser Leu Pro Arg Ser Cys Lys Glu Ile Lys Asp Glu Cys

25 35 40 45
cct agt gca ttt gat ggc ctg tat ttt ctc cgc act gag aat ggt gtt 193
Pro Ser Ala Phe Asp Gly Leu Tyr Phe Leu Arg Thr Glu Asn Gly Val

50 55 60
atc tac cag acc ttc tgt gac atg acc tct ggg ggt ggc ggc tgg acc 241
Ile Tyr Gln Thr Phe Cys Asp Met Thr Ser Gly Gly Gly Gly Trp Thr

65 70 75 80
ctg gtg gcc agc gtg cat gag aat gac atg cgt ggg aag tgc acg gtg 289
Leu Val Ala Ser Val His Glu Asn Asp Met Arg Gly Lys Cys Thr Val

30 85 90 95
ggc gat cgc tgg tcc agt cag cag ggc agc aaa gca gac tac cca gag 337
Gly Asp Arg Trp Ser Ser Gln Gln Gly Ser Lys Ala Asp Tyr Pro Glu

100 105 110
ggg gac ggc aac tgg gcc aac tac aac acc ttt gga tct gca gag gcg 385
Gly Asp Gly Asn Trp Ala Asn Tyr Asn Thr Phe Gly Ser Ala Glu Ala

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	115	120	125	
	gcc acg agc gat gac tac aag aac cct ggc tac tac gac atc cag gcc			433
	Ala Thr Ser Asp Asp Tyr Lys Asn Pro Gly Tyr Tyr Asp Ile Gln Ala			
	130	135	140	
5	aag gac ctg ggc atc tgg cac gtg ccc aat aag tcc ccc atg cag cac			481
	Lys Asp Leu Gly Ile Trp His Val Pro Asn Lys Ser Pro Met Gln His			
	145	150	155	160
	tgg aga aac agc tcc ctg ctg agg tac cgc acg gac act ggc ttc ctc			529
	Trp Arg Asn Ser Ser Leu Leu Arg Tyr Arg Thr Asp Thr Gly Phe Leu			
10	165	170	175	
	cag aca ctg gga cat aat ctg ttt ggc atc tac cag aaa tat cca gtg			577
	Gln Thr Leu Gly His Asn Leu Phe Gly Ile Tyr Gln Lys Tyr Pro Val			
	180	185	190	
	aaa tat gga gaa gga aag tgt tgg act gac aac ggc ccg gtg atc cct			625
15	Lys Tyr Gly Glu Gly Lys Cys Trp Thr Asp Asn Gly Pro Val Ile Pro			
	195	200	205	
	gtg gtc tat gat ttt ggc gac gcc cag aaa aca gca tct tat tac tca			673
	Val Val Tyr Asp Phe Gly Asp Ala Gln Lys Thr Ala Ser Tyr Tyr Ser			
	210	215	220	
20	ccc tat ggc cag cgg gaa ttc act gcg gga ttt gtt cag ttc agg gta			721
	Pro Tyr Gly Gln Arg Glu Phe Thr Ala Gly Phe Val Gln Phe Arg Val			
	225	230	235	240
	ttt aat aac gag aga gca gcc aac gcc ttg tgt gct gga atg agg gtc			769
	Phe Asn Asn Glu Arg Ala Ala Asn Ala Leu Cys Ala Gly Met Arg Val			
25	245	250	255	
	acc gga tgt aac act gag cac cac tgc att ggt gga gga gga tac ttt			817
	Thr Gly Cys Asn Thr Glu His His Cys Ile Gly Gly Gly Tyr Phe			
	260	265	270	
	cca gag gcc agt ccc cag cag tgt gga gat ttt tct ggt ttt gat tgg			865
30	Pro Glu Ala Ser Pro Gln Gln Cys Gly Asp Phe Ser Gly Phe Asp Trp			
	275	280	285	
	agt gga tat gga act cat gtt ggt tac agc agc agc cgt gag ata act			913
	Ser Gly Tyr Gly Thr His Val Gly Tyr Ser Ser Ser Arg Glu Ile Thr			
	290	295	300	
35	gag gca gct gtg ctt cta ttc tat cgt tgagagtttt gtgggagggga			960

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Glu Ala Ala Val Leu Leu Phe Tyr Arg

305

310

accagacct ctctcccaa ccatgagatc ccaaggatgg agaacaactt acccagtagc 1020

tagaatgtta atggcagaag agaaaacaat aaatcatatt gactc 1065

5

<210> 52

<211> 937

<212> DNA

<213> Homo sapiens

10

<220>

<221> CDS

<222> (177)...(866)

<400> 52

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tggagtttct tcagactcca gatttccttg tcaaccacga ggagtccaga gaggaaacgc 120

ggagcggaga caacagtacc tgacgcctct ttcagcccgg gatcgcccca gcaggg 176

atg ggc gac aag atc tgg ctg ccc ttc ccc gtg ctc ctt ctg gcc gct 224

Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala

20

1

5

10

15

ctg cct ccg gtg ctg ctg cct ggg gcg gcc ggc ttc aca cct tcc ctc 272

Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu

20

25

30

gat agc gac ttc acc ttt acc ctt ccc gcc ggc cag aag gag tgc ttc 320

25

Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe

35

40

45

tac cag ccc atg ccc ctg aag gcc tcg ctg gag atc gag tac caa gtt 368

Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val

50

55

60

30

tta gat gga gca gga tta gat att gat ttc cat ctt gcc tct cca gaa 416

Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu

65

70

75

80

ggc aaa acc tta gtt ttt gaa caa aga aaa tca gat gga gtt cac act 464

Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr

35

85

90

95

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	gta gag act gaa gtt ggt gat tac atg ttc tgc ttt gac aat aca ttc	512
	Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe	
	100 105 110	
5	agc acc att tct gag aag gtg att ttc ttt gaa tta atc ctg gat aat	560
	Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn	
	115 120 125	
	atg gga gaa cag gca caa gaa caa gaa gat tgg aag aaa tat att act	608
	Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr	
	130 135 140	
10	ggc aca gat ata ttg gat atg aaa ctg gaa gac atc ctg gaa tcc atc	656
	Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile	
	145 150 155 160	
	aac agc atc aag tcc aga cta agc aaa agt ggg cac ata caa att ctg	704
	Asn Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu	
15	165 170 175	
	ctt aga gca ttt gaa gct cgt gat cga aac ata caa gaa agc aac ttt	752
	Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe	
	180 185 190	
	gat aga gtc aat ttc tgg tct atg gtt aat tta gtg gtc atg gtg gtg	800
20	Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val	
	195 200 205	
	gtg tca gcc att caa gtt tat atg ctg aag agt ctg ttt gaa gat aag	848
	Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys	
	210 215 220	
25	agg aaa agt aga act taaaactcca aactagagta cgtaacattg aaaaatg	900
	Arg Lys Ser Arg Thr	
	225	
	aggcataaaaa atgcaataaaa ctgttacagt caagacc	937
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	<211> 1678	
	<212> DNA	
	<213> Homo sapiens	
	<220>	
35	<221> CDS	

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<222> (56)...(1459)

<400> 53

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5	atg cgg ccc cag gag ctc ccc agg ctc gcg ttc ccg ttg ctg ctg ttg	103
	Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu	
	1 5 10 15	
	ctg ttg ctg ctg ctg ccg ccg ccg ccg tgc cct gcc cac agc gcc acg	151
	Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr	
10	20 25 30	
	cgc ttc gac ccc acc tgg gag tcc ctg gac gcc cgc cag ctg ccc gcg	199
	Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala	
	35 40 45	
	tgg ttt gac cag gcc aag ttc ggc atc ttc atc cac tgg gga gtg ttt	247
15	Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe	
	50 55 60	
	tcc gtg ccc agc ttc ggt agc gag tgg ttc tgg tgg tat tgg caa aag	295
	Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys	
	65 70 75 80	
20	gaa aag ata ccg aag tat gtg gaa ttt atg aaa gat aat tac cct cct	343
	Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro	
	85 90 95	
	agt ttc aaa tat gaa gat ttt gga cca cta ttt aca gca aaa ttt ttt	391
	Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe	
25	100 105 110	
	aat gcc aac cag tgg gca gat att ttt cag gcc tct ggt gcc aaa tac	439
	Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr	
	115 120 125	
	att gtc tta act tcc aaa cat cat gaa ggc ttt acc ttg tgg ggg tca	487
30	Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser	
	130 135 140	
	gaa tat tcg tgg aac tgg aat gcc ata gat gag ggg ccc aag agg gac	535
	Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp	
	145 150 155 160	
35	att gtc aag gaa ctt gag gta gcc att agg aac aga act gac ctg cgt	583

52/177

	Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg	
	165 170 175	
	ttt gga ctg tac tat tcc ctt ttt gaa tgg ttt cat ccg ctc ttc ctt	631
	Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu	
5	180 185 190	
	gag gat gaa tcc agt tca ttc cat aag cgg caa ttt cca gtt tct aag	679
	Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys	
	195 200 205	
	aca ttg cca gag ctc tat gag tta gtg aac aac tat cag cct gag gtt	727
10	Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val	
	210 215 220	
	ctg tgg tcg gat ggt gac gga gga gca ccg gat caa tac tgg aac agc	775
	Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser	
	225 230 235 240	
15	aca ggc ttc ttg gcc tgg tta tat aat gaa agc cca gtt cgg ggc aca	823
	Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr	
	245 250 255	
	gta gtc acc aat gat cgt tgg gga gct ggt agc atc tgt aag cat ggt	871
	Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly	
20	260 265 270	
	ggc ttc tat acc tgc agt gat cgt tat aac cca gga cat ctt ttg cca	919
	Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro	
	275 280 285	
	cat aaa tgg gaa aac tgc atg aca ata gac aaa ctg tcc tgg ggc tat	967
25	His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr	
	290 295 300	
	agg agg gaa gct gga atc tct gac tat ctt aca att gaa gaa ttg gtg	1015
	Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val	
	305 310 315 320	
30	aag caa ctt gta gag aca gtt tca tgt gga gga aat ctt ttg atg aat	1063
	Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn	
	325 330 335	
	att ggg ccc aca cta gat ggc acc att tct gta gtt ttt gag gag cga	1111
	Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg	
35	340 345 350	

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	Leu Arg Gln Met Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr	
	355 360 365	
	gaa acc cat acc tgg cga tcc cag aat gac act gtc acc cca gat gtg	1207
5	Glu Thr His Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val	
	370 375 380	
	tgg tac aca tcc aag cct aaa gaa aaa tta gtc tat gcc att ttt ctt	1255
	Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu	
	385 390 395 400	
10	aaa tgg ccc aca tca gga cag ctg ttc ctt ggc cat ccc aaa gct att	1303
	Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile	
	405 410 415	
	ctg ggg gca aca gag gtg aaa cta ctg ggc cat gga cag cca ctt aac	1351
	Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn	
15	420 425 430	
	tgg att tct ttg gag caa aat ggc att atg gta gaa ctg cca cag cta	1399
	Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu	
	435 440 445	
	acc att cat cag atg ccg tgt aaa tgg ggc tgg gct cta gcc ctg act	1447
20	Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr	
	450 455 460	
	aat gtg atc taaagtgcag cagagtggct gatgctgcaa gttatgtcta aggc	1500
	Asn Val Ile	
	465	
25	taggaactat caggtgtcta taattgtagc acatggagaa agcaaagtga aaactggata	1560
	agaaaattat ttgtgcagtt cagccctttc cctttttccc actaaatttt ttcttaaatt	1620
	acccatgtaa ccattttaac tctccagtgc actttgcat taaagtctct tcacattg	1678
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 cagccagctg agaagagttg agggaaagtg ctgctgctgg gtctgcagac gcg atg 116

5 Met
 1

gat aac gtg cag ccg aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg 164
 Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val

5 10 15

10 aaa ggc cac gtg aag atg ctg cgg ctg gat att atc aac tca ctg gta 212
 Lys Gly His Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val

20 25 30

aca aca gta ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa 260
 Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu

15 35 40 45

acc aca aca ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca 308
 Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala

50 55 60 65

gta tgc tgt ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc 356
 Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe

20 70 75 80

aat ccc agc ggt cct tac cag caa aag cct gtg cat gaa aaa aaa gaa 404
 Asn Pro Ser Gly Pro Tyr Gln Gln Lys Pro Val His Glu Lys Lys Glu

85 90 95

25 gtt ttg taattttata ttacttttta gtttgatact aagtattaaa 450
 Val Leu

catatttctg tattctt 467

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	gggtgctgcg gattgaggtc ccggttccta acgaatctct gctggattgg ccgtaaccct	180
	gtccccgagc gggctcacag ggtctgaagg ccacgcata ggcaaaggta aagttctgag	240
	ccaccgggtg cctccttccc aggaactcaa g atg gag gaa ggc ggg aac cta	292
	Met Glu Glu Gly Gly Asn Leu	
10	1 5	
	gga ggc ctg att aag atg gtc cat cta ctg gtc ttg tca ggt gcc tgg	340
	Gly Gly Leu Ile Lys Met Val His Leu Leu Val Leu Ser Gly Ala Trp	
	10 15 20	
	ggc atg caa atg tgg gtg acc ttc gtc tca ggc ttc ctg ctt ttc cga	388
15	Gly Met Gln Met Trp Val Thr Phe Val Ser Gly Phe Leu Leu Phe Arg	
	25 30 35	
	agc ctt ccc cga cat acc ttc gga cta gtg cag agc aaa ctc ttc ccc	436
	Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys Leu Phe Pro	
	40 45 50 55	
20	ttc tac ttc cac atc tcc atg ggc tgt gcc ttc atc aac ctc tgc atc	484
	Phe Tyr Phe His Ile Ser Met Gly Cys Ala Phe Ile Asn Leu Cys Ile	
	60 65 70	
	ttg gct tca cag cat gct tgg gct cag ctc aca ttc tgg gag gcc agc	532
	Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser	
25	75 80 85	
	cag ctt tac ctg ctg ttc ctg agc ctt acg ctg gcc act gtc aac gcc	580
	Gln Leu Tyr Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr Val Asn Ala	
	90 95 100	
	cgc tgg ctg gaa ccc cgc acc aca gct gcc atg tgg gcc ctg caa acc	628
30	Arg Trp Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala Leu Gln Thr	
	105 110 115	
	gtg gag aag gag cga ggc ctg ggt ggg gag gta cca ggc agc cac cag	676
	Val Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly Ser His Gln	
	120 125 130 135	
35	ggc ccc gat ccc tac cgc cag ctg cga gag aag gac ccc aag tac agt	724

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Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro Lys Tyr Ser
 140 145 150
 gct ctc cgc cag aat ttc ttc cgc tac cat ggg ctg tcc tct ctt tgc 772
 Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser Ser Leu Cys
 5 155 160 165
 aat ctg ggc tgc gtc ctg agc aat ggg ctc tgt ctc gct ggc ctt gcc 820
 Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala Gly Leu Ala
 170 175 180
 ctg gaa ata agg agc ctc tagcatgggc cctgcatgct aataaatgct tcttcag 875
 10 Leu Glu Ile Arg Ser Leu
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 atattggagc caacactcca gatgctacaa aaggctgtcc agatgtccaa gcttccttgc 120
 cagatgccaa agccaagtcc ccaccgacc atg gtg gac agc ctc ctg gca gtc 173
 25 Met Val Asp Ser Leu Leu Ala Val
 1 5
 acc ctg gct gga aac ctg ggc ctg acc ttc ctc cga ggt tcc cag acc 221
 Thr Leu Ala Gly Asn Leu Gly Leu Thr Phe Leu Arg Gly Ser Gln Thr
 10 15 20
 30 cag agc cat cca gac ctg gga act gag ggc tgc tgg gac cag ctc tct 269
 Gln Ser His Pro Asp Leu Gly Thr Glu Gly Cys Trp Asp Gln Leu Ser
 25 30 35 40
 gcc cct cgg acc ttt acg ctt ttg gac ccc aag gca tct ctg tta acc 317
 Ala Pro Arg Thr Phe Thr Leu Leu Asp Pro Lys Ala Ser Leu Leu Thr
 35 45 50 55

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	aag gcc ttc ctc aat ggc gcc ctg gat ggg gtc atc ctt gga gac tac	365
	Lys Ala Phe Leu Asn Gly Ala Leu Asp Gly Val Ile Leu Gly Asp Tyr	
	60 65 70	
	ctg agc cgg act cct gag ccc cgg cca tcc ctc agc cac ttg ctg agc	413
5	Leu Ser Arg Thr Pro Glu Pro Arg Pro Ser Leu Ser His Leu Leu Ser	
	75 80 85	
	cag tac tat ggg gct ggg gtg gcc aga gac cca ggg ttc cgc agc aac	461
	Gln Tyr Tyr Gly Ala Gly Val Ala Arg Asp Pro Gly Phe Arg Ser Asn	
	90 95 100	
10	ttc cga cgg cag aac ggt gct gct ctg act tca gcc tcc atc ctg gcc	509
	Phe Arg Arg Gln Asn Gly Ala Ala Leu Thr Ser Ala Ser Ile Leu Ala	
	105 110 115 120	
	cag cag gtg tgg gga acc ctt gtc ctt cta cag agg ctg gag cca gta	557
	Gln Gln Val Trp Gly Thr Leu Val Leu Leu Gln Arg Leu Glu Pro Val	
15	125 130 135	
	cac ctc cag ctt cag tgc atg agc caa gaa cag ctg gcc cag gtg gct	605
	His Leu Gln Leu Gln Cys Met Ser Gln Glu Gln Leu Ala Gln Val Ala	
	140 145 150	
	gcc aat gct acc aag gaa ttc act gag gcc ttc ctg gga tgc ccg gcc	653
20	Ala Asn Ala Thr Lys Glu Phe Thr Glu Ala Phe Leu Gly Cys Pro Ala	
	155 160 165	
	atc cac ccc cgc tgc cgc tgg gga gcg gcg cct tat cgg ggc cgc ccg	701
	Ile His Pro Arg Cys Arg Trp Gly Ala Ala Pro Tyr Arg Gly Arg Pro	
	170 175 180	
25	aag ctg ctg cag ctg ccg ctg gga ttc ttg tac gtg cat cac acc tac	749
	Lys Leu Leu Gln Leu Pro Leu Gly Phe Leu Tyr Val His His Thr Tyr	
	185 190 195 200	
	gtg cct gca cca ccc tgc acg gac ttc acg cgc tgc gca gcc aac atg	797
	Val Pro Ala Pro Pro Cys Thr Asp Phe Thr Arg Cys Ala Ala Asn Met	
30	205 210 215	
	cgc tcc atg cag cgc tac cac cag gac acg caa ggc tgg gga gac atc	845
	Arg Ser Met Gln Arg Tyr His Gln Asp Thr Gln Gly Trp Gly Asp Ile	
	220 225 230	
	ggc tac agt ttc gtg gtg ggc tcg gac ggc tac gtg tac gag gga cgc	893
35	Gly Tyr Ser Phe Val Val Gly Ser Asp Gly Tyr Val Tyr Glu Gly Arg	

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	235	240	245	
	ggc tgg cac tgg gtg ggc gcc cac acg ctc ggc cac aac tcc cgg ggc			941
	Gly Trp His Trp Val Gly Ala His Thr Leu Gly His Asn Ser Arg Gly			
	250	255	260	
5	ttc ggc gtg gcc ata gtg ggc aac tac acc gcg gcg ctg ccc acc gag			989
	Phe Gly Val Ala Ile Val Gly Asn Tyr Thr Ala Ala Leu Pro Thr Glu			
	265	270	275	280
	gcc gct ctg cgc acg gtg cgc gac acg ctc ccg agt tgt gcg gtg cgc			1037
	Ala Ala Leu Arg Thr Val Arg Asp Thr Leu Pro Ser Cys Ala Val Arg			
10		285	290	295
	gcc ggc ctc ctg cgg cca gac tac gcg ctg ctg ggc cac cgc cag ctg			1085
	Ala Gly Leu Leu Arg Pro Asp Tyr Ala Leu Leu Gly His Arg Gln Leu			
	300	305	310	
	gtg cgc acc gac tgc ccc ggc gac gcg ctc ttc gac ctg ctg cgc acc			1133
15	Val Arg Thr Asp Cys Pro Gly Asp Ala Leu Phe Asp Leu Leu Arg Thr			
	315	320	325	
	tgg ccg cac ttc acc gcg act gtt aag cca aga cct gcc agg agt gtc			1181
	Trp Pro His Phe Thr Ala Thr Val Lys Pro Arg Pro Ala Arg Ser Val			
	330	335	340	
20	tct aag aga tcc agg agg gag cca ccc cca agg acc ctg cca gcc aca			1229
	Ser Lys Arg Ser Arg Arg Glu Pro Pro Pro Arg Thr Leu Pro Ala Thr			
	345	350	355	360
	gac ctc caa taaagacagc atggaaac			1256
	Asp Leu Gln			
25				
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	<211> 884			
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	<400> 57			
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	gctggagacc tccgcgtgg cccccgcgag cctcctgcc tggcccggcg ctgcggtct	120
	gccgcggcgg cagc atg ggt ggc ccc cgg ggc gcg ggc tgg gtg gcg gcg	170
	Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala	
	1 5 10	
5	ggc ctg ctg ctc ggc gcg ggc gcc tgc tac tgc att tac agg ctg acc	218
	Gly Leu Leu Leu Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr	
	15 20 25	
	cgg ggt cgg cgg cgg ggc gac cgc gag ctc ggg ata cgc tct tcg aag	266
	Arg Gly Arg Arg Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys	
10	30 35 40	
	tcc gca gaa gac tta act gat ggt tca tat gat gat gtt cta aat gct	314
	Ser Ala Glu Asp Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala	
	45 50 55 60	
	gaa caa ctt cag aaa ctc ctt tac ctg ctg gag tca acg gag gat cct	362
15	Glu Gln Leu Gln Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro	
	65 70 75	
	gta att att gaa aga gct ttg att act ttg ggt aac aat gca gcc ttt	410
	Val Ile Ile Glu Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe	
	80 85 90	
20	tca gtt aac caa gct att att cgt gaa ttg ggt ggt att cca att gtt	458
	Ser Val Asn Gln Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val	
	95 100 105	
	gca aac aaa atc aac cat tcc aac cag agt att aaa gag aaa gct tta	506
	Ala Asn Lys Ile Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu	
25	110 115 120	
	aat gca cta aat aac ctg agt gtg aat gtt gaa aat caa atc aag ata	554
	Asn Ala Leu Asn Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile	
	125 130 135 140	
	aag gtg caa gtt ttg aaa ctg ctt ttg aat ttg tct gaa aat cca gcc	602
30	Lys Val Gln Val Leu Lys Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala	
	145 150 155	
	atg aca gaa gga ctt ctc cgt gcc caa gtg gat tca tca ttc ctt tcc	650
	Met Thr Glu Gly Leu Leu Arg Ala Gln Val Asp Ser Ser Phe Leu Ser	
	160 165 170	
35	ctt tat gac agc cac gta gca aag gag att ctt ctt cga gta ctt acg	698

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Leu Tyr Asp Ser His Val Ala Lys Glu Ile Leu Leu Arg Val Leu Thr
 175 180 185
 cta ttt cag aat ata aag aac tgc ctc aaa ata gaa ggc cat tta gct 746
 Leu Phe Gln Asn Ile Lys Asn Cys Leu Lys Ile Glu Gly His Leu Ala
 5 190 195 200
 gtg cag cct act ttc act gaa ggt tca ttg ttt ttc ctg tta cat gga 794
 Val Gln Pro Thr Phe Thr Glu Gly Ser Leu Phe Phe Leu Leu His Gly
 205 210 215 220
 gaa gaa tgt gcc cag aaa ata aga gct tta gtt gat cac cat gat gca 842
 10 Glu Glu Cys Ala Gln Lys Ile Arg Ala Leu Val Asp His His Asp Ala
 225 230 235
 gag gtg aag gaa aag gtt gta aca ata ata ccc aaa atc tga 884
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 240 245
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 20 <220>
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 Met Ala Ser
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 Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile Val Leu Ser
 30 5 10 15
 gcc tgg gga gtg atc atg ttg ata atg ctc gga ata ttt ttc aat gtc 152
 Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val
 20 25 30 35
 cat tcc gct gtg ttg att gag gac gtt ccc ttc acg gag aaa gat ttt 200
 35 His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu Lys Asp Phe

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	40	45	50	
	gag aat ggc ccc cag aac ata tac aac ctt tac gag caa gtc agc tac			248
	Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu Gln Val Ser Tyr			
	55	60	65	
5	aac tgt ttc atc gct gca ggc ctt tac ctc ctc ctc gga ggc ttc tct			296
	Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Leu Gly Gly Phe Ser			
	70	75	80	
	ttc tgc caa gtt cgg ctc aat aag cgc aag gaa tac atg gtg cgc			341
	Phe Cys Gln Val Arg Leu Asn Lys Arg Lys Glu Tyr Met Val Arg			
10	85	90	95	
	tagggcccc ggcgcgtttc cccgcctccag cccctcctct atttaaagac tccctgcacc			400
	gtgtcaccoca ggtegcgtcc cacccttgcc ggcgcctct gtgggactgg gtttcccg			460
	cgagagactg aatcccttct cccatctctg gcacccggcc cccgtggaga gggctgaggc			520
	tggggggctg ttccgtctct ccacccttcg ctgtgtcccg tatctcaata aagagaatct			580
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	Met Val Gly Pro Ala Pro Arg Arg Arg			
	1	5		
	ctg cgg cgg ctg gca gcg ctg gcc ctg gtc ctg gcg ctg gcc cgg ggg			99
30	Leu Arg Pro Leu Ala Ala Leu Ala Leu Val Leu Ala Leu Ala Pro Gly			
	10	15	20	25
	ctg ccc aca gcc cgg gcc ggg cag aca ccg cgc cct gcc gag cgg ggg			147
	Leu Pro Thr Ala Arg Ala Gly Gln Thr Pro Arg Pro Ala Glu Arg Gly			
	30	35	40	
35	ccc cca gtg cgg ctt ttc acc gag gag gag ctg gcc cgc tat ggc ggg			195

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Pro Pro Val Arg Leu Phe Thr Glu Glu Glu Leu Ala Arg Tyr Gly Gly
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 gag gag gaa gat cag ccc atc tac ttg gca gtg aag gga gtg gtg ttt 243
 Glu Glu Glu Asp Gln Pro Ile Tyr Leu Ala Val Lys Gly Val Val Phe
 5 60 65 70
 gat gtc acc tcc gga aag gag ttt tat gga cga gga gcc ccc tac aat 291
 Asp Val Thr Ser Gly Lys Glu Phe Tyr Gly Arg Gly Ala Pro Tyr Asn
 75 80 85
 gcc ttg acg ggg aag gac tcc act aga ggg gta gcc aag atg tcc ttg 339
 10 Ala Leu Thr Gly Lys Asp Ser Thr Arg Gly Val Ala Lys Met Ser Leu
 90 95 100 105
 gat cct gca gac ctc acc cat gac act acg ggt ctc acg gcc aag gaa 387
 Asp Pro Ala Asp Leu Thr His Asp Thr Thr Gly Leu Thr Ala Lys Glu
 110 115 120
 15 ctg gag gcc ctg gat gag gtc ttc acc aaa gtg tac aaa gcc aaa tac 435
 Leu Glu Ala Leu Asp Glu Val Phe Thr Lys Val Tyr Lys Ala Lys Tyr
 125 130 135
 ccc atc gtc ggc tac act gcc cgg aga att ctc aat gag gat ggc agc 483
 Pro Ile Val Gly Tyr Thr Ala Arg Arg Ile Leu Asn Glu Asp Gly Ser
 20 140 145 150
 cct aac ctg gac ttc aag cct gaa gac cag ccc cat ttt gac atc aag 531
 Pro Asn Leu Asp Phe Lys Pro Glu Asp Gln Pro His Phe Asp Ile Lys
 155 160 165
 gat gag ttc tgatgttccc cctgcaggag caggttcttg ggagcgtgag 580
 25 Asp Glu Phe
 170
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	cgtgtt atg atg ccg tcc cgt acc aac ctg gct act gga atc ccc agt	168
	Met Met Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser	
	1 5 10	
	agt aaa gtg aaa tat tca agg ctc tcc agc aca gac gat ggc tac att	216
10	Ser Lys Val Lys Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile	
	15 20 25 30	
	gac ctt cag ttt aag aaa acc cct cct aag atc cct tat aag gcc atc	264
	Asp Leu Gln Phe Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile	
	35 40 45	
15	gca ctt gcc act gtg ctg ttt ttg att ggc gcc ttt ctc att att ata	312
	Ala Leu Ala Thr Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile	
	50 55 60	
	ggc tcc ctc ctg ctg tca ggc tac atc agc aaa ggg ggg gca gac cgg	360
	Gly Ser Leu Leu Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg	
20	65 70 75	
	gcc gtt cca gtg ctg atc att ggc att ctg gtg ttc cta ccc gga ttt	408
	Ala Val Pro Val Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe	
	80 85 90	
	tac cac ctg cgc atc gct tac tat gca tcc aaa ggc tac cgt ggt tac	456
25	Tyr His Leu Arg Ile Ala Tyr Tyr Ala Ser Lys Gly Tyr Arg Gly Tyr	
	95 100 105 110	
	tcc tat gat gac att cca gac ttt gat gac tagcaccac ccca	500
	Ser Tyr Asp Asp Ile Pro Asp Phe Asp Asp	
	115 120	
30	tagctgagga ggagtcacag tggaaactgtc ccagctttaa gatattctagc agaaactata	560
	gctgaggact aaggaattct gcagcttgca gatgtttaag aaaataatgg ccagattttt	620
	tgggtccttc ccaaagatgt taagtgaacc tacagttagc taattaggac aagctctatt	680
	tttcatccct gggccctgac aagtttttcc acaggaatat gtatcatgga agaatagagg	740
	ttattctgta atggaaaagt gttgcctgcc accaccctct gtagagctga gcatttcttt	800
35	taaatagtct tcattgccaa tttgttcttg tagcaaatgg aacaatgtgg tatggcta	860

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 cctaccttca tgttccagtg gaagacctta gtaaaatcaa agatcagtga gttcatctgt 980
 aatatttttt ttacttgctt tcttactgac agcaaccagg aattttttta tctgcagag 1040
 caagttttca aaatgtaaata acttcctctg tttaacagtc cttggaccat tctgatccag 1100
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<211> 307

<212> PRT

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<400> 61

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 20 25 30
 Cys Arg Lys Tyr Phe Lys Met Leu Ser Arg Lys Leu Ala Gln Leu Pro
 35 40 45
 Asp Arg Cys Thr Leu Lys Thr Gly His Tyr Asn Ile Asn Phe Ile Ser
 25 50 55 60
 Ser Leu Gly Val Ser Tyr Met Met Leu Cys Thr Glu Asn Tyr Pro Asn
 65 70 75 80
 Val Leu Ala Phe Ser Phe Leu Asp Glu Leu Gln Lys Glu Phe Ile Thr
 85 90 95
 30 Thr Tyr Asn Met Met Lys Thr Asn Thr Ala Val Arg Pro Tyr Cys Phe
 100 105 110
 Ile Glu Phe Asp Asn Phe Ile Gln Arg Thr Lys Gln Arg Tyr Asn Asn
 115 120 125
 Pro Arg Ser Leu Ser Thr Lys Ile Asn Leu Ser Asp Met Gln Thr Glu
 35 130 135 140

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Ile Lys Leu Arg Pro Pro Tyr Gln Ile Ser Met Cys Glu Leu Gly Ser
 145 150 155 160
 Ala Asn Gly Val Thr Ser Ala Phe Ser Val Asp Cys Lys Gly Ala Gly
 165 170 175
 5 Lys Ile Ser Ser Ala His Gln Arg Leu Glu Pro Ala Thr Leu Ser Gly
 180 185 190
 Ile Val Gly Phe Ile Leu Ser Leu Leu Cys Gly Ala Leu Asn Leu Ile
 195 200 205
 Arg Gly Phe His Ala Ile Glu Ser Leu Leu Gln Ser Asp Gly Asp Asp
 10 210 215 220
 Phe Asn Tyr Ile Ile Ala Phe Phe Leu Gly Thr Ala Ala Cys Leu Tyr
 225 230 235 240
 Gln Cys Tyr Leu Leu Val Tyr Tyr Thr Gly Trp Arg Asn Val Lys Ser
 245 250 255
 15 Phe Leu Thr Phe Gly Leu Ile Cys Leu Cys Asn Met Tyr Leu Tyr Glu
 260 265 270
 Leu Arg Asn Leu Trp Gln Leu Phe Phe His Val Thr Val Gly Ala Phe
 275 280 285
 Val Thr Leu Gln Ile Trp Leu Arg Gln Ala Gln Gly Lys Ala Pro Asp
 20 290 295 300
 Tyr Asp Val
 305

 <210> 62
 25 <211> 183
 <212> PRT
 <213> Homo sapiens

 <400> 62
 30 Met Thr Ala Gln Gly Gly Leu Val Ala Asn Arg Gly Arg Arg Phe Lys
 1 5 10 15
 Trp Ala Ile Glu Leu Ser Gly Pro Gly Gly Gly Ser Arg Gly Arg Ser
 20 25 30
 Asp Arg Gly Ser Gly Gln Gly Asp Ser Leu Tyr Pro Val Gly Tyr Leu
 35 35 40 45

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Asp Lys Gln Val Pro Asp Thr Ser Val Gln Glu Thr Asp Arg Ile Leu
 50 55 60
 Val Glu Lys Arg Cys Trp Asp Ile Ala Leu Gly Pro Leu Lys Gln Ile
 65 70 75 80
 5 Pro Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr Ile Ser Ile
 85 90 95
 Phe Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro Ile Gln Ala
 100 105 110
 Leu Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser Ser Ser Gln
 10 115 120 125
 Lys Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu Met Gly Leu
 130 135 140
 Ala Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu Pro Thr His
 145 150 155 160
 15 Ala Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg Met Glu Phe
 165 170 175
 Ser Gly Gly Gly Leu Leu Leu
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 20 <210> 63
 <211> 327
 <212> PRT
 <213> Homo sapiens
 25 <400> 63
 Met Arg Ala Leu Pro Gly Leu Leu Glu Ala Arg Ala Arg Thr Pro Arg
 1 5 10 15
 Leu Leu Leu Leu Gln Cys Leu Leu Ala Ala Ala Arg Pro Ser Ser Ala
 20 25 30
 30 Asp Gly Ser Ala Pro Asp Ser Pro Phe Thr Ser Pro Pro Leu Arg Glu
 35 40 45
 Glu Ile Met Ala Asn Asn Phe Ser Leu Glu Ser His Asn Ile Ser Leu
 50 55 60
 Thr Glu His Ser Ser Met Pro Val Glu Lys Asn Ile Thr Leu Glu Arg
 35 65 70 75 80

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Pro Ser Asn Val Asn Leu Thr Cys Gln Phe Thr Thr Ser Gly Asp Leu
85 90 95
Asn Ala Val Asn Val Thr Trp Lys Lys Asp Gly Glu Gln Leu Glu Asn
100 105 110
5 Asn Tyr Leu Val Ser Ala Thr Gly Ser Thr Leu Tyr Thr Gln Tyr Arg
115 120 125
Phe Thr Ile Ile Asn Ser Lys Gln Met Gly Ser Tyr Ser Cys Phe Phe
130 135 140
Arg Glu Glu Lys Glu Gln Arg Gly Thr Phe Asn Phe Lys Val Pro Glu
10 145 150 155 160
Leu His Gly Lys Asn Lys Pro Leu Ile Ser Tyr Val Gly Asp Ser Thr
165 170 175
Val Leu Thr Cys Lys Cys Gln Asn Cys Phe Pro Leu Asn Trp Thr Trp
180 185 190
15 Tyr Ser Ser Asn Gly Ser Val Lys Val Pro Val Gly Val Gln Met Asn
195 200 205
Lys Tyr Val Ile Asn Gly Thr Tyr Ala Asn Glu Thr Lys Leu Lys Ile
210 215 220
Thr Gln Leu Leu Glu Glu Asp Gly Glu Ser Tyr Trp Cys Arg Ala Leu
20 225 230 235 240
Phe Gln Leu Gly Glu Ser Glu Glu His Ile Glu Leu Val Val Leu Ser
245 250 255
Tyr Leu Val Pro Leu Lys Pro Phe Leu Val Ile Val Ala Glu Val Ile
260 265 270
25 Leu Leu Val Ala Thr Ile Leu Leu Cys Glu Lys Tyr Thr Gln Lys Lys
275 280 285
Lys Lys His Ser Asp Glu Gly Lys Glu Phe Glu Gln Ile Glu Gln Leu
290 295 300
Lys Ser Asp Asp Ser Asn Gly Ile Glu Asn Asn Val Pro Arg His Arg
30 305 310 315 320
Lys Asn Glu Ser Leu Gly Gln
325

<210> 64

35 <211> 223

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<212> PRT

<213> Homo sapiens

<400> 64

5 Met Lys Phe Val Pro Cys Leu Leu Leu Val Thr Leu Ser Cys Leu Gly
1 5 10 15
Thr Leu Gly Gln Ala Pro Arg Gln Lys Gln Gly Ser Thr Gly Glu Glu
20 25 30
Phe His Phe Gln Thr Gly Gly Arg Asp Ser Cys Thr Met Arg Pro Ser
10 35 40 45
Ser Leu Gly Gln Gly Ala Gly Glu Val Trp Leu Arg Val Asp Cys Arg
50 55 60
Asn Thr Asp Gln Thr Tyr Trp Cys Glu Tyr Arg Gly Gln Pro Ser Met
65 70 75 80
15 Cys Gln Ala Phe Ala Ala Asp Pro Lys Ser Tyr Trp Asn Gln Ala Leu
85 90 95
Gln Glu Leu Arg Arg Leu His His Ala Cys Gln Gly Ala Pro Val Leu
100 105 110
Arg Pro Ser Val Cys Arg Glu Ala Gly Pro Gln Ala His Met Gln Gln
20 115 120 125
Val Thr Ser Ser Leu Lys Gly Ser Pro Glu Pro Asn Gln Gln Pro Glu
130 135 140
Ala Gly Thr Pro Ser Leu Arg Pro Lys Ala Thr Val Lys Leu Thr Glu
145 150 155 160
25 Ala Thr Gln Leu Gly Lys Asp Ser Met Glu Glu Leu Gly Lys Ala Lys
165 170 175
Pro Thr Thr Arg Pro Thr Ala Lys Pro Thr Gln Pro Gly Pro Arg Pro
180 185 190
Gly Gly Asn Glu Glu Ala Lys Lys Lys Ala Trp Glu His Cys Trp Lys
30 195 200 205
Pro Phe Gln Ala Leu Cys Ala Phe Leu Ile Ser Phe Phe Arg Gly
210 215 220

<210> 65

35 <211> 48

69/177

<212> PRT

<213> Homo sapiens

<400> 65

5 Met Arg Leu Leu Leu Leu Leu Val Ala Ala Ser Ala Met Val Arg
 1 5 10 15
 Ser Glu Ala Ser Ala Asn Leu Gly Gly Val Pro Ser Lys Arg Leu Lys
 20 25 30
 Met Gln Tyr Ala Thr Gly Pro Leu Leu Lys Phe Gln Ile Cys Val Ser
 10 35 40 45

<210> 66

<211> 371

<212> PRT

15 <213> Homo sapiens

<400> 66

Met Ala Trp Thr Lys Tyr Gln Leu Phe Leu Ala Gly Leu Met Leu Val
 1 5 10 15
 20 Thr Gly Ser Ile Asn Thr Leu Ser Ala Lys Trp Ala Asp Asn Phe Met
 20 25 30
 Ala Glu Gly Cys Gly Gly Ser Lys Glu His Ser Phe Gln His Pro Phe
 35 40 45
 Leu Gln Ala Val Gly Met Phe Leu Gly Glu Phe Ser Cys Leu Ala Ala
 25 50 55 60
 Phe Tyr Leu Leu Arg Cys Arg Ala Ala Gly Gln Ser Asp Ser Ser Val
 65 70 75 80
 Asp Pro Gln Gln Pro Phe Asn Pro Leu Leu Phe Leu Pro Pro Ala Leu
 85 90 95
 30 Cys Asp Met Thr Gly Thr Ser Leu Met Tyr Val Ala Leu Asn Met Thr
 100 105 110
 Ser Ala Ser Ser Phe Gln Met Leu Arg Gly Ala Val Ile Ile Phe Thr
 115 120 125
 Gly Leu Phe Ser Val Ala Phe Leu Gly Arg Arg Leu Val Leu Ser Gln
 35 130 135 140

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Trp Leu Gly Ile Leu Ala Thr Ile Ala Gly Leu Val Val Val Gly Leu
145 150 155 160
Ala Asp Leu Leu Ser Lys His Asp Ser Gln His Lys Leu Ser Glu Val
165 170 175
5 Ile Thr Gly Asp Leu Leu Ile Ile Met Ala Gln Ile Ile Val Ala Ile
180 185 190
Gln Met Val Leu Glu Glu Lys Phe Val Tyr Lys His Asn Val His Pro
195 200 205
Leu Arg Ala Val Gly Thr Glu Gly Leu Phe Gly Phe Val Ile Leu Ser
10 210 215 220
Leu Leu Leu Val Pro Met Tyr Tyr Ile Pro Ala Gly Ser Phe Ser Gly
225 230 235 240
Asn Pro Arg Gly Thr Leu Glu Asp Ala Leu Asp Ala Phe Cys Gln Val
245 250 255
15 Gly Gln Gln Pro Leu Ile Ala Val Ala Leu Leu Gly Asn Ile Ser Ser
260 265 270
Ile Ala Phe Phe Asn Phe Ala Gly Ile Ser Val Thr Lys Glu Leu Ser
275 280 285
Ala Thr Thr Arg Met Val Leu Asp Ser Leu Arg Thr Val Val Ile Trp
20 290 295 300
Ala Leu Ser Leu Ala Leu Gly Trp Glu Ala Phe His Ala Leu Gln Ile
305 310 315 320
Leu Gly Phe Leu Ile Leu Leu Ile Gly Thr Ala Leu Tyr Asn Gly Leu
325 330 335
25 His Arg Pro Leu Leu Gly Arg Leu Ser Arg Gly Arg Pro Leu Ala Glu
340 345 350
Glu Ser Glu Gln Glu Arg Leu Leu Gly Gly Thr Arg Thr Pro Ile Asn
355 360 365
Asp Ala Ser
30 370

<210> 67

<211> 90

<212> PRT

35 <213> Homo sapiens

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<400> 67

Met Phe His Gln Ile Trp Ala Ala Leu Leu Tyr Phe Tyr Gly Ile Ile
 1 5 10 15
 5 Leu Asn Ser Ile Tyr Gln Cys Pro Glu His Ser Gln Leu Thr Thr Leu
 20 25 30
 Gly Val Asp Gly Lys Glu Phe Pro Glu Val His Leu Gly Gln Trp Tyr
 35 40 45
 Phe Ile Ala Gly Ala Ala Pro Thr Lys Glu Glu Leu Ala Thr Phe Asp
 10 50 55 60
 Pro Val Asp Asn Ile Val Phe Asn Met Ala Ala Gly Ser Ala Pro Met
 65 70 75 80
 Gln Leu His Leu Arg Ala Thr Ile Arg Met
 85 90

15

<210> 68

<211> 499

<212> PRT

<213> Homo sapiens

20

<400> 68

Met Val Asp Arg Gly Pro Leu Leu Thr Ser Ala Ile Ile Phe Tyr Leu
 1 5 10 15
 Ala Ile Gly Ala Ala Ile Phe Glu Val Leu Glu Glu Pro His Trp Lys
 25 20 25 30
 Glu Ala Lys Lys Asn Tyr Tyr Thr Gln Lys Leu His Leu Leu Lys Glu
 35 40 45
 Phe Pro Cys Leu Gly Gln Glu Gly Leu Asp Lys Ile Leu Glu Val Val
 50 55 60
 30 Ser Asp Ala Ala Gly Gln Gly Val Ala Ile Thr Gly Asn Gln Thr Phe
 65 70 75 80
 Asn Asn Trp Asn Trp Pro Asn Ala Met Ile Phe Ala Ala Thr Val Ile
 85 90 95
 Thr Thr Ile Gly Tyr Gly Asn Val Ala Pro Lys Thr Pro Ala Gly Arg
 35 100 105 110

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Leu Phe Cys Val Phe Tyr Gly Leu Phe Gly Val Pro Leu Cys Leu Thr
 115 120 125
 Trp Ile Ser Ala Leu Gly Lys Phe Phe Gly Gly Arg Ala Lys Arg Leu
 130 135 140
 5 Gly Gln Phe Leu Thr Lys Arg Gly Val Ser Leu Arg Lys Ala Gln Ile
 145 150 155 160
 Thr Cys Thr Val Ile Phe Ile Val Trp Gly Val Leu Val His Leu Val
 165 170 175
 Ile Pro Pro Phe Val Phe Met Val Thr Glu Gly Trp Asn Tyr Ile Glu
 10 180 185 190
 Gly Leu Tyr Tyr Ser Phe Ile Thr Ile Ser Thr Ile Gly Phe Gly Asp
 195 200 205
 Phe Val Ala Gly Val Asn Pro Ser Ala Asn Tyr His Ala Leu Tyr Arg
 210 215 220
 15 Tyr Phe Val Glu Leu Trp Ile Tyr Leu Gly Leu Ala Trp Leu Ser Leu
 225 230 235 240
 Phe Val Asn Trp Lys Val Ser Met Phe Val Glu Val His Lys Ala Ile
 245 250 255
 Lys Lys Arg Arg Arg Arg Arg Lys Glu Ser Phe Glu Ser Ser Pro His
 20 260 265 270
 Ser Arg Lys Ala Leu Gln Val Lys Gly Ser Thr Ala Ser Lys Asp Val
 275 280 285
 Asn Ile Phe Ser Phe Leu Ser Lys Lys Glu Glu Thr Tyr Asn Asp Leu
 290 295 300
 25 Ile Lys Gln Ile Gly Lys Lys Ala Met Lys Thr Ser Gly Gly Gly Glu
 305 310 315 320
 Thr Gly Pro Gly Pro Gly Leu Gly Pro Gln Gly Gly Gly Leu Pro Ala
 325 330 335
 Leu Pro Pro Ser Leu Val Pro Leu Val Val Tyr Ser Lys Asn Arg Val
 30 340 345 350
 Pro Thr Leu Glu Glu Val Ser Gln Thr Leu Arg Ser Lys Gly His Val
 355 360 365
 Ser Arg Ser Pro Asp Glu Glu Ala Val Ala Arg Ala Pro Glu Asp Ser
 370 375 380
 35 Ser Pro Ala Pro Glu Val Phe Met Asn Gln Leu Asp Arg Ile Ser Glu

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385 390 395 400
 Glu Cys Glu Pro Trp Asp Ala Gln Asp Tyr His Pro Leu Ile Phe Gln
 405 410 415
 Asp Ala Ser Ile Thr Phe Val Asn Thr Glu Ala Gly Leu Ser Asp Glu
 5 420 425 430
 Glu Thr Ser Lys Ser Ser Leu Glu Asp Asn Leu Ala Gly Glu Glu Ser
 435 440 445
 Pro Gln Gln Gly Ala Glu Ala Lys Ala Pro Leu Asn Met Gly Glu Phe
 450 455 460
 10 Pro Ser Ser Ser Glu Ser Thr Phe Thr Ser Thr Glu Ser Glu Leu Ser
 465 470 475 480
 Val Pro Tyr Glu Gln Leu Met Asn Glu Tyr Asn Lys Ala Asn Ser Pro
 485 490 495
 Lys Gly Thr
 15

 <210> 69
 <211> 106
 <212> PRT
 20 <213> Homo sapiens

 <400> 69
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 25 Ala Pro Phe Ala Gln Arg Ile Asp Pro Thr Arg Glu Lys Leu Thr Pro
 20 25 30
 Glu Gln Leu His Ser Met Arg Gln Ala Glu Leu Ala Gln Trp Gln Lys
 35 40 45
 Val Leu Pro Arg Arg Arg Thr Arg Asn Ile Val Thr Gly Leu Gly Ile
 30 50 55 60
 Gly Ala Leu Val Leu Ala Ile Tyr Gly Tyr Thr Phe Tyr Ser Ile Ser
 65 70 75 80
 Gln Glu Arg Phe Leu Asp Glu Leu Glu Asp Glu Ala Lys Ala Ala Arg
 85 90 95
 35 Ala Arg Ala Leu Ala Arg Ala Ser Gly Ser

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100

105

<210> 70

<211> 152

5 <212> PRT

<213> Homo sapiens

<400> 70

Met Asp Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp
10 1 5 10 15
Glu Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu
20 25 30
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly Ile
35 40 45
15 Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp Lys Lys
50 55 60
Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly Arg Pro Glu
65 70 75 80
Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His Glu Asp Ala Leu
20 85 90 95
Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe Pro Asp Val Ser Gly
100 105 110
Val Ser Arg Ile Pro Ser Arg Ser Val Pro Ala Ser Asp Cys Val Ser
115 120 125
25 Gly Gln Asp Leu His Ser Thr Val Tyr Glu Val Ile Gln His Ile Pro
130 135 140
Ala Gln Gln Gln Asp His Pro Glu
145 150

30 <210> 71

<211> 921

<212> DNA

<213> Homo sapiens

35 <400> 71

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 tcgaggaaaac ttgctcaact tcctgataga tgtacactga aaactggaca ttataacatt 180
 aattttatta gctctctggg agtgagctac atgatgttgt gcaactgaaaa ttacccaaat 240
 5 gttctcgccct tctctttcct ggatgagctt cagaaggagt tcattactac ttataacatg 300
 atgaagacaa atactgctgt cagaccatac tgtttcattg aatttgataa cttcattcag 360
 aggaccaagc agcgatataa taatcccagg tctctttcaa caaagataaa tctttctgac 420
 atgcagacgg aaatcaagct gaggcctcct tatcaaattt ccatgtgcga actgggggtca 480
 gccaatggag tcacatcagc attttctgtt gactgtaaag gtgctggtaa gatttcttct 540
 10 gctcaccagc gactggaacc agcaactctg tcagggattg taggatttat ccttagtctt 600
 ttatgtggag ctctgaattt aattcgaggc tttcatgcta tagaaagtct cctgcagagt 660
 gatggtgatg attttaatta catcattgca ttttctcttg gaacagcagc ctgcctttac 720
 cagtgttatt tacttgtcta ctacaccggc tggcggaatg tcaaactctt tttgactttt 780
 ggcttaatat gtctatgcaa catgtatctc tatgaactgc gcaacctctg gcagcttttc 840
 15 tttcatgtga ctgtgggagc atttgttaca ctacagatct ggctaaggca agcccagggc 900
 aaggetcccg attatgatgt c 921

<210> 72

<211> 549

20 <212> DNA

<213> Homo sapiens

<400> 72

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 tcgctctacc cagtcgggta cttggacaag caagtgcctg ataccagcgt gcaagagaca 180
 gaccggatcc tgggtggagaa gcgctgctgg gacatcgcc tgggtcccct caaacagatt 240
 cccatgaatc tcttcatcat gtacatggca ggcaatacta tctccatctt cctactatg 300
 atggtgtgta tgatggcctg ggcacccatt caggcaacta tggccatttc agccatttc 360
 30 aagatgttag aaagttcaag ccagaagttt cttcaggggt tgggtctatct cattgggaac 420
 ctgatgggtt tggcattggc tgtttacaag tgccagtcca tgggactgtt acctacacat 480
 gcatcggatt ggttagcctt cattgagccc cctgagagaa tggagtccag tgggtggagga 540
 ctgcttttg 549

35 <210> 73

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<211> 981

<212> DNA

<213> Homo sapiens

5

<400> 73

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	cagtgccttc	tcgctgccgc	gcgcccgaagc	tcggcggacg	gcagtgcctc	agattcgcct	120
	tttacaagtc	cacctctcag	agaagaaata	atggcaaata	acttttcctt	ggagagtcac	180
	aacatatcac	tgactgaaca	ttctagtatg	ccagtagaaa	aaaatatcac	tttagaaagg	240
10	cctttctaag	ttaaattcac	atgccagttc	acaacatctg	gggatttgaa	tgcagtaaag	300
	gtgacttgga	aaaaagatgg	tgaacaactt	gagaataatt	atcttgtcag	tgcaacagga	360
	agcaccttgt	ataccaata	caggttcacc	atcattaata	gcaaacaagt	gggaagttat	420
	tcttgtttct	ttcgagagga	aaaggaacaa	aggggaacat	ttaatttcaa	agtccctgaa	480
	cttcattgga	aaaacaagcc	attgatctct	tacgtagggg	attctactgt	cttgacatgt	540
15	aaatgtcaaa	attgttttcc	tttaaatggg	acctgggtaca	gtagtaattg	gagtgtaaag	600
	gttcctgttg	gtgttcaaat	gaataaatat	gtgatcaatg	gaacatatgc	taacgaaaca	660
	aagctgaaga	taacacaact	tttggaggaa	gatggggaat	cttactgggtg	ccgtgcacta	720
	ttccaattag	gcgagagtga	agaacacatt	gagcttggtg	tgctgagcta	tttgggtgcc	780
	ctcaaaccat	ttcttgtaat	agtggctgag	gtgattcttt	tagtgccac	cattctgctt	840
20	tgtgaaaagt	acacacaaaa	gaaaaagaag	cactcagatg	aggggaaaga	atttgagcag	900
	attgaacagc	tgaaatcaga	tgatagcaat	ggtatagaaa	ataatgtccc	caggcataga	960
	aaaaatgagt	ctctgggcca	g				981

<210> 74

25

<211> 669

<212> DNA

<213> Homo sapiens

<400> 74

30

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	gattcctgca	ctatgcgtcc	cagcagcttg	gggcaagggtg	ctggagaagt	ctggcttcgc	180
	gtcgactgcc	gcaacacaga	ccagacctac	tggtgtgagt	acagggggca	gccagcatg	240
	tgccaggett	tcgctgctga	ccccaaatct	tactgggaatc	aagccctgca	ggagctgagg	300
35	cgccttcacc	atgcgtgcc	ggggggccccg	gtgcttaggc	catccgtgtg	cagggaggct	360

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	ggaccccagg cccatatgca gcaggtgact tccagcctca agggcagccc agagcccaac	420
	cagcagcctg aggctgggac gccatctctg aggcccaagg ccacagtga actcacagaa	480
	gcaacacagc tgggaaagga ctogatggaa gagctgggaa aagccaaacc caccaccoga	540
	cccacagcca aacctaccca gcctggaccc agggccggag ggaatgagga agcaaagaag	600
5	aaggcctggg aacattgttg gaaacccttc caggccctgt gcgcctttct catcagcttc	660
	ttccgaggg	669
	<210> 75	
	<211> 144	
10	<212> DNA	
	<213> Homo sapiens	
	<400> 75	
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	ctcaagttec agatttgtgt ttec	144
	<210> 76	
	<211> 1113	
20	<212> DNA	
	<213> Homo sapiens	
	<400> 76	
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	gagcacagct tccagcatcc ctctctccag gcagtgggca tgttctctgg agaattctcc	180
	tgcttggtct ccttctacct cctccgatgc agagctgcag ggcaatcaga ctccagcgta	240
	gacccccagc agcccttcaa cctcttcttt ttcttgcccc cagcgtctct tgacatgaca	300
	gggaccagcc tcatgtatgt ggctctgaac atgaccagt cctccagctt ccagatgctg	360
30	cgggggtgcag tgatcatatt cactggcctg ttctcggtgg ccttctctgg ccggaggctg	420
	gtgctgagcc agtggctggg catcctagcc accatcgagg ggctgggtgg cgtgggctg	480
	gctgacctcc tgagcaagca cgacagtcag cacaagctca gcgaagtgat cacaggggac	540
	ctgttgatca tcatggccca gatcctcgtt gccatccaga tgggtgctaga ggagaagttc	600
	gtctacaaac acaatgtgca cccactgagg gcagttggca ctgagggcct ctttggcttt	660
35	gtgatcctct cctgctgct ggtgcccatt tactacatcc ccgccggctc cttcagcgga	720

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	aacctcgtg ggacaactgga ggatgcattg gacgccttct gccaggtggg ccagcagcgg	780
	ctcattgccg tggcactgct gggcaacatc agcagcattg ccttcttcaa cttcgcaggc	840
	atcagcgtca ccaaggaact gagcgccacc acccgcatgg tgttggacag cttgcgcacc	900
	gttgtcatct gggcactgag cctggcactg ggctgggagg ccttccatgc actgcagatc	960
5	cttggcttcc tcatactect tataggcact gccctctaca atgggctaca ccgtccgctg	1020
	ctgggcccgc tgtccagggg ccggccccctg gcagaggaga gcgagcagga gagactgctg	1080
	ggtggcaccg gcactcccat caatgatgcc agc	1113
	<210> 77	
10	<211> 270	
	<212> DNA	
	<213> Homo sapiens	
	<400> 77	
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	taccagtgcc ctgagcacag tcaactgaca actctgggag tggatgggaa ggagttccca	120
	gaggctccact tgggcccagt gtactttatc gcaggggcag cccccaccaa ggaggagttg	180
	gcaacttttg acctgtgga caacattgtc ttcaatatgg ctgctggctc tgccccgatg	240
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20	<210> 78	
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	<212> DNA	
	<213> Homo sapiens	
25	<400> 78	
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	cagaagctgc atctgtctaa ggagttcccg tgctgggtc aggagggcct ggacaagatc	180
30	ctagaggtgg tatctgatgc tgcaggacag ggtgtggcca tcacaggga ccagaccttc	240
	aacaactgga actggcccaa tgcaatgatt tttgcagcga ccgtcattac caccattgga	300
	tatggcaatg tggtcccaa gacccccgcg ggctgcctct tctgtgtttt ctatggtctc	360
	ttcgggggtgc cgtctctgct gacgtggatc agtgccttg gcaagttctt cgggggacgt	420
	gccaaagagac tagggcagtt ccttaccagg agaggtgtga gtctgcggaa ggcgcagatc	480
35	acgtgcacag tcattctcat cgtgtggggc gtctagtc acctggtgat cccacccttc	540

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gtattcatgg tgactgaggg gtggaactac atcgagggcc tctactactc cttcatcacc 600
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 gccctgtacc gctacttcgt ggagctctgg atctacttgg ggctggcctg gctgtccctt 720
 tttgtcaact ggaaggtgag catgtttgtg gaagtccaca aagccattaa gaagcggcgg 780
 5 cggcgacgga aggagtcctt tgagagctcc ccacactccc ggaaggccct gcaggtgaag 840
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 tacaacgacc tcatcaagca gatcgggaag aaggccatga agacaagcgg ggggtggggag 960
 acggggcccg gccagggct ggggcctcaa ggcggtgggc tcccagcact gccccttcc 1020
 ctggtgcccc tggtagtcta ctccaagaac cgggtgcccc ccttggaaga ggtgtcacag 1080
 10 aactgagga gcaaaggcca cgtatcaagg tcccagatg aggaggctgt ggcacgggcc 1140
 cctgaagaca gctccccctgc ccccgaggtg ttcatgaacc agctggaccg catcagcgag 1200
 gaatgcgagc catgggacgc ccaggactac caccactca tcttccagga cgccagcatc 1260
 accttcgtga acacggaggc tggcctctca gacgaggaga cctccaagtc ctgcgtagag 1320
 gacaacttgg caggggagga gagccccag cagggggctg aagccaaggc gcccctgaac 1380
 15 atgggcgagt tcccctctc ctccagctcc accttcacca gcaactgagtc tgagctctct 1440
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<211> 318

20 <212> DNA

<213> Homo sapiens

<400> 79

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 25 cagcgtatcg acccgactcg ggagaagctg acaccgagc aactgcattc catgcggcag 120
 gcggagcttg cccagtgga gaaggctcta ccacggcggc gaaccgggaa catcgtgacc 180
 ggcctaggca tcggggccct ggtgttggt atttatggtt acaccttcta ctgatttcc 240
 caggagcgtt tctagatga gctagaagac gaggccaaag ctgcccagc ccgagctctg 300
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30

<210> 80

<211> 456

<212> DNA

<213> Homo sapiens

35

80/177

<400> 80

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acagttatca tcaactccgt aggactggag aagcttgac agaaaggaaa atcattgtca 120
ccttttagcaa gtataactgg aatatcacta tttttgatta tatccatgtg tcttctcttc 180
5 ctatggaaaa aatatcaacc ctacaaagt ataaaacaga aactagaagg caggccagaa 240
acagaataca ggaaagctca aacattttca ggccatgaag atgctctgga tgacttcgga 300
atatatgaat ttgttgcttt tccagatgtt tctggtgttt ccaggatccc aagcaggtct 360
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cagcacatcc ctgcccagca gcaagaccat ccagag 456

10

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<211> 1436
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<222> (66)...(989)

<400> 81

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ttgaa atg tct atg att tta tct gcc tca gtc att cgt gtc aga gat 107
Met Ser Met Ile Leu Ser Ala Ser Val Ile Arg Val Arg Asp
1 5 10

gga ctg cca ctt tct gct tct act gat tat gaa caa agc aca gga atg 155
25 Gly Leu Pro Leu Ser Ala Ser Thr Asp Tyr Glu Gln Ser Thr Gly Met
15 20 25 30

cag gag tgc aga aag tat ttt aaa atg ctt tcg agg aaa ctt gct caa 203
Gln Glu Cys Arg Lys Tyr Phe Lys Met Leu Ser Arg Lys Leu Ala Gln
35 40 45

30 ctt cct gat aga tgt aca ctg aaa act gga cat tat aac att aat ttt 251
Leu Pro Asp Arg Cys Thr Leu Lys Thr Gly His Tyr Asn Ile Asn Phe
50 55 60

att agc tct ctg gga gtg agc tac atg atg ttg tgc act gaa aat tac 299
Ile Ser Ser Leu Gly Val Ser Tyr Met Met Leu Cys Thr Glu Asn Tyr

35 65 70 75

81/177

	cca aat gtt ctc gcc ttc tct ttc ctg gat gag ctt cag aag gag ttc	347
	Pro Asn Val Leu Ala Phe Ser Phe Leu Asp Glu Leu Gln Lys Glu Phe	
	80 85 90	
	att act act tat aac atg atg aag aca aat act gct gtc aga cca tac	395
5	Ile Thr Thr Tyr Asn Met Met Lys Thr Asn Thr Ala Val Arg Pro Tyr	
	95 100 105 110	
	tgt ttc att gaa ttt gat aac ttc att cag agg acc aag cag cga tat	443
	Cys Phe Ile Glu Phe Asp Asn Phe Ile Gln Arg Thr Lys Gln Arg Tyr	
	115 120 125	
10	aat aat ccc agg tct ctt tca aca aag ata aat ctt tct gac atg cag	491
	Asn Asn Pro Arg Ser Leu Ser Thr Lys Ile Asn Leu Ser Asp Met Gln	
	130 135 140	
	acg gaa atc aag ctg agg cct cct tat caa att tcc atg tgc gaa ctg	539
	Thr Glu Ile Lys Leu Arg Pro Pro Tyr Gln Ile Ser Met Cys Glu Leu	
15	145 150 155	
	ggg tca gcc aat gga gtc aca tca gca ttt tct gtt gac tgt aaa ggt	587
	Gly Ser Ala Asn Gly Val Thr Ser Ala Phe Ser Val Asp Cys Lys Gly	
	160 165 170	
	gct ggt aag att tct tct gct cac cag cga ctg gaa cca gca act ctg	635
20	Ala Gly Lys Ile Ser Ser Ala His Gln Arg Leu Glu Pro Ala Thr Leu	
	175 180 185 190	
	tca ggg att gta gga ttt atc ctt agt ctt tta tgt gga gct ctg aat	683
	Ser Gly Ile Val Gly Phe Ile Leu Ser Leu Leu Cys Gly Ala Leu Asn	
	195 200 205	
25	tta att cga ggc ttt cat gct ata gaa agt ctc ctg cag agt gat ggt	731
	Leu Ile Arg Gly Phe His Ala Ile Glu Ser Leu Leu Gln Ser Asp Gly	
	210 215 220	
	gat gat ttt aat tac atc att gca ttt ttc ctt gga aca gca gcc tgc	779
	Asp Asp Phe Asn Tyr Ile Ile Ala Phe Phe Leu Gly Thr Ala Ala Cys	
30	225 230 235	
	ctt tac cag tgt tat tta ctt gtc tac tac acc ggc tgg cgg aat gtc	827
	Leu Tyr Gln Cys Tyr Leu Leu Val Tyr Tyr Thr Gly Trp Arg Asn Val	
	240 245 250	
	aaa tct ttt ttg act ttt ggc tta atc tgt cta tgc aac atg tat ctc	875
35	Lys Ser Phe Leu Thr Phe Gly Leu Ile Cys Leu Cys Asn Met Tyr Leu	

82/177

	255	260	265	270	
	tat gaa ctg cgc aac ctc tgg cag ctt ttc ttt cat gtg act gtg gga				923
	Tyr Glu Leu Arg Asn Leu Trp Gln Leu Phe Phe His Val Thr Val Gly				
		275	280	285	
5	gca ttt gtt aca cta cag atc tgg cta agg caa gcc cag ggc aag gct				971
	Ala Phe Val Thr Leu Gln Ile Trp Leu Arg Gln Ala Gln Gly Lys Ala				
		290	295	300	
	ccc gat tat gat gtc tgacaccatc cttcagatct attgccttgg ctte				1020
	Pro Asp Tyr Asp Val				
10		305			
	agggggataa ggagggaaca tatcataact gcactgtgat gaagaagctg ttccccacag				1080
	aggagaagct ctgctttctt tctctccaac tttccttttt taaaatcagc atgatgtgcc				1140
	tgtgagcatg gaagagtcct ctcagaagaa tgttggccat gagactatca ttcagaggag				1200
	gaggggattt ctctcttcaa ggccataaca gtggaagaac agtcatatgc cattggaagt				1260
15	cttgccagc agtcctgaat ccttctgaa gagttcagaa aatagatgtg gtattgctct				1320
	gaggaccagg caggaggaac totacaacct gagtttgcc ttgtgaggca ttagtataga				1380
	ccaaataaaa agctgcagaa attggaaagt ttatgtttta aataaatgac tgtgat				1436
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	cgaggctata ggacgcagct gttgcc atg acg gcc cag ggg ggc ctg gtg				110
30	Met Thr Ala Gln Gly Gly Leu Val				
		1	5		
	gct aac cga ggc cgg cgc ttc aag tgg gcc att gag cta agc ggg cct				158
	Ala Asn Arg Gly Arg Arg Phe Lys Trp Ala Ile Glu Leu Ser Gly Pro				
		10	15	20	
35	gga gga ggc agc agg ggt cga agt gac cgg ggc agt ggc cag gga gac				206

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	Gly Gly Gly Ser Arg Gly Arg Ser Asp Arg Gly Ser Gly Gln Gly Asp	
	25 30 35 40	
	tcg ctc tac cca gtc ggt tac ttg gac aag caa gtg cct gat acc agc	254
5	Ser Leu Tyr Pro Val Gly Tyr Leu Asp Lys Gln Val Pro Asp Thr Ser	
	45 50 55	
	gtg caa gag aca gac cgg atc ctg gtg gag aag cgc tgc tgg gac atc	302
	Val Gln Glu Thr Asp Arg Ile Leu Val Glu Lys Arg Cys Trp Asp Ile	
	60 65 70	
10	gcc ttg ggt ccc ctc aaa cag att ccc atg aat ctc ttc atc atg tac	350
	Ala Leu Gly Pro Leu Lys Gln Ile Pro Met Asn Leu Phe Ile Met Tyr	
	75 80 85	
	atg gca ggc aat act atc tcc atc ttc cct act atg atg gtg tgt atg	398
	Met Ala Gly Asn Thr Ile Ser Ile Phe Pro Thr Met Met Val Cys Met	
	90 95 100	
15	atg gcc tgg cga ccc att cag gca ctt atg gcc att tca gcc act ttc	446
	Met Ala Trp Arg Pro Ile Gln Ala Leu Met Ala Ile Ser Ala Thr Phe	
	105 110 115 120	
	aag atg tta gaa agt tca agc cag aag ttt ctt cag ggt ttg gtc tat	494
	Lys Met Leu Glu Ser Ser Ser Gln Lys Phe Leu Gln Gly Leu Val Tyr	
20	125 130 135	
	ctc att ggg aac ctg atg ggt ttg gca ttg gct gtt tac aag tgc cag	542
	Leu Ile Gly Asn Leu Met Gly Leu Ala Leu Ala Val Tyr Lys Cys Gln	
	140 145 150	
25	tcc atg gga ctg tta cct aca cat gca tcg gat tgg tta gcc ttc att	590
	Ser Met Gly Leu Leu Pro Thr His Ala Ser Asp Trp Leu Ala Phe Ile	
	155 160 165	
	gag ccc cct gag aga atg gag ttc agt ggt gga gga ctg ctt ttg tgaac	640
	Glu Pro Pro Glu Arg Met Glu Phe Ser Gly Gly Gly Leu Leu Leu	
	170 175 180	
30	atgagaaagc agcgccctggt ccctatgtat ttgggtctta tttacatcct tctttaagcc	700
	cagtggctcc tcagcatact cttaaactaa tcacttatgt taaaaagaac caaaagactc	760
	ttttctccat ggtgggggtga caggtcctag aaggacaatg tgcatattac gacaaacaca	820
	aagaaactat accataacc aaggctgaaa ataatgtaga aaactttatt tttgtttcca	880
	gtacagagca aaacaacaac aaaaaaacat aactatgtaa acaagagaat aactgctgct	940
35	aaatcaagaa ctgtttgcagc atctccttcc aataaattaa atggttgaga acaatgc	997

84/177

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 <211> 1753
 <212> DNA
 5 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (134)...(1117)

10 <400> 83
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 gggactctgg acaccgcgg cggcgagctg agggagcagt ctccacgagg acccaggcgg 120
 accctctggc gcc atg cgc gcc ctc ccc ggc ctg ctg gag gcc agg gcg 169
 Met Arg Ala Leu Pro Gly Leu Leu Glu Ala Arg Ala
 15 1 5 10
 cgt acg ccc cgg ctg ctc ctc ctc cag tgc ctt ctc gct gcc gcg cgc 217
 Arg Thr Pro Arg Leu Leu Leu Leu Gln Cys Leu Leu Ala Ala Ala Arg
 15 20 25
 cca agc tcg gcg gac ggc agt gcc cca gat tcg cct ttt aca agt cca 265
 20 Pro Ser Ser Ala Asp Gly Ser Ala Pro Asp Ser Pro Phe Thr Ser Pro
 30 35 40
 cct ctc aga gaa gaa ata atg gca aat aac ttt tcc ttg gag agt cat 313
 Pro Leu Arg Glu Glu Ile Met Ala Asn Asn Phe Ser Leu Glu Ser His
 45 50 55 60
 25 aac ata tca ctg act gaa cat tct agt atg cca gta gaa aaa aat atc 361
 Asn Ile Ser Leu Thr Glu His Ser Ser Met Pro Val Glu Lys Asn Ile
 65 70 75
 act tta gaa agg cct tct aat gta aat ctc aca tgc cag ttc aca aca 409
 Thr Leu Glu Arg Pro Ser Asn Val Asn Leu Thr Cys Gln Phe Thr Thr
 30 80 85 90
 tct ggg gat ttg aat gca gta aat gtg act tgg aaa aaa gat ggt gaa 457
 Ser Gly Asp Leu Asn Ala Val Asn Val Thr Trp Lys Lys Asp Gly Glu
 95 100 105
 caa ctt gag aat aat tat ctt gtc agt gca aca gga agc acc ttg tat 505
 35 Gln Leu Glu Asn Asn Tyr Leu Val Ser Ala Thr Gly Ser Thr Leu Tyr

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	110	115	120	
	acc caa tac agg ttc acc atc att aat agc aaa caa atg gga agt tat	553		
	Thr Gln Tyr Arg Phe Thr Ile Ile Asn Ser Lys Gln Met Gly Ser Tyr			
	125	130	135	140
5	tct tgt ttc ttt cga gag gaa aag gaa caa agg gga aca ttt aat ttc	601		
	Ser Cys Phe Phe Arg Glu Glu Lys Glu Gln Arg Gly Thr Phe Asn Phe			
	145	150	155	
	aaa gtc cct gaa ctt cat ggg aaa aac aag cca ttg atc tct tac gta	649		
	Lys Val Pro Glu Leu His Gly Lys Asn Lys Pro Leu Ile Ser Tyr Val			
10	160	165	170	
	ggg gat tct act gtc ttg aca tgt aaa tgt caa aat tgt ttt cct tta	697		
	Gly Asp Ser Thr Val Leu Thr Cys Lys Cys Gln Asn Cys Phe Pro Leu			
	175	180	185	
	aat tgg acc tgg tac agt agt aat ggg agt gta aag gtt cct gtt ggt	745		
15	Asn Trp Thr Trp Tyr Ser Ser Asn Gly Ser Val Lys Val Pro Val Gly			
	190	195	200	
	gtt caa atg aat aaa tat gtg atc aat gga aca tat gct aac gaa aca	793		
	Val Gln Met Asn Lys Tyr Val Ile Asn Gly Thr Tyr Ala Asn Glu Thr			
	205	210	215	220
20	aag ctg aag ata aca caa ctt ttg gag gaa gat ggg gaa tct tac tgg	841		
	Lys Leu Lys Ile Thr Gln Leu Leu Glu Glu Asp Gly Glu Ser Tyr Trp			
	225	230	235	
	tgc cgt gca cta ttc caa tta ggc gag agt gaa gaa cac att gag ctt	889		
	Cys Arg Ala Leu Phe Gln Leu Gly Glu Ser Glu Glu His Ile Glu Leu			
25	240	245	250	
	gtg gtg ctg agc tat ttg gtg ccc ctc aaa cca ttt ctt gta ata gtg	937		
	Val Val Leu Ser Tyr Leu Val Pro Leu Lys Pro Phe Leu Val Ile Val			
	255	260	265	
	gct gag gtg att ctt tta gtg gcc acc att ctg ctt tgt gaa aag tac	985		
30	Ala Glu Val Ile Leu Leu Val Ala Thr Ile Leu Leu Cys Glu Lys Tyr			
	270	275	280	
	aca caa aag aaa aag aag cac tca gat gag ggg aaa gaa ttt gag cag	1033		
	Thr Gln Lys Lys Lys Lys His Ser Asp Glu Gly Lys Glu Phe Glu Gln			
	285	290	295	300
35	att gaa cag ctg aaa tca gat gat agc aat ggt ata gaa aat aat gtc	1081		

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Ile Glu Gln Leu Lys Ser Asp Asp Ser Asn Gly Ile Glu Asn Asn Val
 305 310 315
 ccc agg cat aga aaa aat gag tct ctg ggc cag tgaatacaaa acatca 1130
 Pro Arg His Arg Lys Asn Glu Ser Leu Gly Gln
 5 320 325
 tgtcgagaat cattggaaga tatacagagt tcgtatttca gctttattta tccttcctgt 1190
 taagagcctc tgagttttta gttttaaaag gatgaaaagc ttatgcaaca tgctcagcag 1250
 gagcttcac c aacgatatat gtcagatcta aaggtatatt ttcattctgt aattatgtta 1310
 cataaaagca atgtaaatca gaataaatat gttagaccag aataaaaatta attatattct 1370
 10 ggtcttcaaa ggacacacag aacagatata agcagaatca ctttaatactt catagaacaa 1430
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 gtcttagaaa gttatttttt taaaaaaaaat catacttact attagtattct atggaagtat 1550
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 aagttgaaat gaatactttc tgccttttgc catgatagtt attctacaat ctccacaaga 1670
 15 aaaatatacc ttttatccgg aaatattggt ttaaggcaaa taaataaaac tgtgcttgc 1730
 ctaaagctct gcactacaaa agc 1753

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 20 <212> DNA
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 <222> (62)...(733)

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 c atg aag ttc gtc ccc tgc etc ctg ctg gtg acc ttg tcc tgc ctg 106
 Met Lys Phe Val Pro Cys Leu Leu Leu Val Thr Leu Ser Cys Leu
 30 1 5 10 15
 ggg act ttg ggt cag gcc ccg agg caa aag caa gga agc act ggg gag 154
 Gly Thr Leu Gly Gln Ala Pro Arg Gln Lys Gln Gly Ser Thr Gly Glu
 20 25 30
 gaa ttc cat ttc cag act gga ggg aga gat tcc tgc act atg cgt ccc 202
 35 Glu Phe His Phe Gln Thr Gly Gly Arg Asp Ser Cys Thr Met Arg Pro

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	35	40	45	
	agc agc ttg ggg caa ggt gct gga gaa gtc tgg ctt cgc gtc gac tgc	250		
	Ser Ser Leu Gly Gln Gly Ala Gly Glu Val Trp Leu Arg Val Asp Cys			
	50	55	60	
5	cgc aac aca gac cag acc tac tgg tgt gag tac agg ggg cag ccc agc	298		
	Arg Asn Thr Asp Gln Thr Tyr Trp Cys Glu Tyr Arg Gly Gln Pro Ser			
	65	70	75	
	atg tgc cag gct ttc gct gct gac ccc aaa tct tac tgg aat caa gcc	346		
	Met Cys Gln Ala Phe Ala Ala Asp Pro Lys Ser Tyr Trp Asn Gln Ala			
10	80	85	90	95
	ctg cag gag ctg agg cgc ctt cac cat gcg tgc cag ggg gcc ccg gtg	394		
	Leu Gln Glu Leu Arg Arg Leu His His Ala Cys Gln Gly Ala Pro Val			
	100	105	110	
	ctt agg cca tcc gtg tgc agg gag gct gga ccc cag gcc cat atg cag	442		
15	Leu Arg Pro Ser Val Cys Arg Glu Ala Gly Pro Gln Ala His Met Gln			
	115	120	125	
	cag gtg act tcc agc ctc aag ggc agc cca gag ccc aac cag cag cct	490		
	Gln Val Thr Ser Ser Leu Lys Gly Ser Pro Glu Pro Asn Gln Gln Pro			
	130	135	140	
20	gag gct ggg acg cca tct ctg agg ccc aag gcc aca gtg aaa ctc aca	538		
	Glu Ala Gly Thr Pro Ser Leu Arg Pro Lys Ala Thr Val Lys Leu Thr			
	145	150	155	
	gaa gca aca cag ctg gga aag gac tcg atg gaa gag ctg gga aaa gcc	586		
	Glu Ala Thr Gln Leu Gly Lys Asp Ser Met Glu Glu Leu Gly Lys Ala			
25	160	165	170	175
	aaa ccc acc acc cga ccc aca gcc aaa cct acc cag cct gga ccc agg	634		
	Lys Pro Thr Thr Arg Pro Thr Ala Lys Pro Thr Gln Pro Gly Pro Arg			
	180	185	190	
	ccc gga ggg aat gag gaa gca aag aag aag gcc tgg gaa cat tgt tgg	682		
30	Pro Gly Gly Asn Glu Glu Ala Lys Lys Lys Ala Trp Glu His Cys Trp			
	195	200	205	
	aaa ccc ttc cag gcc ctg tgc gcc ttt ctc atc agc ttc ttc cga ggg	730		
	Lys Pro Phe Gln Ala Leu Cys Ala Phe Leu Ile Ser Phe Phe Arg Gly			
	210	215	220	
35	tgacaggtga aagaccccta cagatctgac ctctccctga cagacaacca tctcttttta	790		

88/177

	tattatgccg ctttcaatcc aacgttctca cactggaaga agagagtttc taatcagatg	850
	caacggccca aattcttgat ctgcagcttc tctgaagttt ggaaaagaaa ccttcctttc	910
	tggagtttgc agagttcagc aatatgatag ggaacaggtg ctgatgggcc caagagtgc	970
	aagcatacac aactacttat tatctgtaga agttttgctt tgttgatctg agccttctat	1030
5	gaaagtttaa atatgtaacg cattcatgaa tttccagtgt tcagtaaata gcagctatgt	1090
	gtgtgcaaaa taaaagaatg atttcag	1117
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	<211> 1380	
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	<213> Homo sapiens	
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	<222> (43)...(189)	
15	<400> 85	
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	Met Arg Leu Leu	
	1	
20	ctg ctt ctc cta gtg gcg gcg tct gcg atg gtc cgg agc gag gcc tcg	102
	Leu Leu Leu Leu Val Ala Ala Ser Ala Met Val Arg Ser Glu Ala Ser	
	5 10 15 20	
	gcc aat ctg gcc gcc gtg ccc agc aag aga tta aag atg cag tac gcc	150
	Ala Asn Leu Gly Gly Val Pro Ser Lys Arg Leu Lys Met Gln Tyr Ala	
25	25 30 35	
	acg ggg ccg ctg ctc aag ttc cag att tgt gtt tcc tgag	190
	Thr Gly Pro Leu Leu Lys Phe Gln Ile Cys Val Ser	
	40 45	
	gttataggcg ggtgtttgag gagtacatgc gggttattag ccagcgggtac ccagacatcc	250
30	gcattgaagg agagaattac ctccctcaac caatatatag acacatagca tctttcctgt	310
	cagtcttcaa actagtatta ataggcttaa taattgttgg caaggatcct tttgctttct	370
	ttggcatgca agctcctagc atctggcagt ggggccaaga aaataagggtt tatgcatgta	430
	tgatggtttt cttcttgagc aacatgattg agaaccagtg tatgtcaaca ggtgcatttg	490
	agataacttt aaatgatgta cctgtgtggt ctaagctgga atctgggtcac cttccatcca	550
35	tgcaacaact tgttcaaatt cttgacaatg aaatgaagct caatgtgcat atggattcaa	610

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	tcccacacca tcgatcatag caccacotat cagcactgaa aactcttttg cattaagggga	670
	tcattgcaag agcagcgtga ctgacattat gaaggcctgt actgaagaca gcaagctggt	730
	agtacagacc agatgctttc ttggcagget cgttgtacct cttggaaaac ctcaatgcaa	790
	gatagtgttt cagtgtctggc atatttttggga attctgcaca ttcattggagt gcaataatac	850
5	tgtatagctt tcccacctc ccacaaaate acccagttaa tgtgtgtgtg tgtttttttt	910
	tttaaggtaa acattactac ttgtaacttt tttcttagt catatttgaa aaagtagaaa	970
	attgagttac aatttgattt tttttccaaa gatgtctgtt aaatctgttg tgcttttata	1030
	tgaatatttg ttttttatag tttaaaattg atcctttggg aatccagttg aagttcccaa	1090
	atactttata agagttttatc agacatctct aatttggcca tgtccagttt atacagttta	1150
10	caaaatatag cagatgcaag attatggggg aaatcctata ttcagagtac tctataaatt	1210
	tttgtgtatg tgtgtatgtg cgtgtgatta ccagagaact actaaaaaaaa ccaactgctt	1270
	tttaaatect attgtgtagt taaagtgtca tgccttgacc aatctaataga attgattaat	1330
	taactggggc tttatactta actaaataaa aaactaagca gatatgagtt	1380
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	<212> DNA	
	<213> Homo sapiens	
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	<400> 86	
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	Met Ala	
	1	
	tgg acc aag tac cag ctg ttc ctg gcc ggg ctc atg ctt gtt acc ggc	104
	Trp Thr Lys Tyr Gln Leu Phe Leu Ala Gly Leu Met Leu Val Thr Gly	
	5 10 15	
30	tcc atc aac acg ctc tcg gca aaa tgg gcg gac aat ttc atg gcc gag	152
	Ser Ile Asn Thr Leu Ser Ala Lys Trp Ala Asp Asn Phe Met Ala Glu	
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	ggc tgt gga ggg agc aag gag cac agc ttc cag cat ccc ttc ctc cag	200
	Gly Cys Gly Gly Ser Lys Glu His Ser Phe Gln His Pro Phe Leu Gln	
35	35 40 45 50	

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	Ala Val Gly Met Phe Leu Gly Glu Phe Ser Cys Leu Ala Ala Phe Tyr	
	55 60 65	
	ctc ctc cga tgc aga gct gca ggg caa tca gac tcc agc gta gac ccc	296
5	Leu Leu Arg Cys Arg Ala Ala Gly Gln Ser Asp Ser Ser Val Asp Pro	
	70 75 80	
	cag cag ccc ttc aac cct ctt ctt ttc ctg ccc cca gcg ctc tgt gac	344
	Gln Gln Pro Phe Asn Pro Leu Leu Phe Leu Pro Pro Ala Leu Cys Asp	
	85 90 95	
10	atg aca ggg acc agc ctc atg tat gtg gct ctg aac atg acc agt gcc	392
	Met Thr Gly Thr Ser Leu Met Tyr Val Ala Leu Asn Met Thr Ser Ala	
	100 105 110	
	tcc agc ttc cag atg ctg cgg ggt gca gtg atc ata ttc act ggc ctg	440
	Ser Ser Phe Gln Met Leu Arg Gly Ala Val Ile Ile Phe Thr Gly Leu	
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	ttc tcg gtg gcc ttc ctg ggc cgg agg ctg gtg ctg agc cag tgg ctg	488
	Phe Ser Val Ala Phe Leu Gly Arg Arg Leu Val Leu Ser Gln Trp Leu	
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	ctc ctg agc aag cac gac agt cag cac aag ctc agc gaa gtg atc aca	584
	Leu Leu Ser Lys His Asp Ser Gln His Lys Leu Ser Glu Val Ile Thr	
	165 170 175	
25	ggg gac ctg ttg atc atc atg gcc cag atc atc gtt gcc atc cag atg	632
	Gly Asp Leu Leu Ile Ile Met Ala Gln Ile Ile Val Ala Ile Gln Met	
	180 185 190	
	gtg cta gag gag aag ttc gtc tac aaa cac aat gtg cac cca ctg cgg	680
	Val Leu Glu Glu Lys Phe Val Tyr Lys His Asn Val His Pro Leu Arg	
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	gca gtt ggc act gag ggc ctc ttt ggc ttt gtg atc ctc tcc ctg ctg	728
	Ala Val Gly Thr Glu Gly Leu Phe Gly Phe Val Ile Leu Ser Leu Leu	
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	Arg Gly Thr Leu Glu Asp Ala Leu Asp Ala Phe Cys Gln Val Gly Gln			
	245	250	255	
5	cag ccg ctc att gcc gtg gca ctg ctg ggc aac atc agc agc att gcc			872
	Gln Pro Leu Ile Ala Val Ala Leu Leu Gly Asn Ile Ser Ser Ile Ala			
	260	265	270	
	ttc ttc aac ttc gca ggc atc agc gtc acc aag gaa ctg agc gcc acc			920
	Phe Phe Asn Phe Ala Gly Ile Ser Val Thr Lys Glu Leu Ser Ala Thr			
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	acc cgc atg gtg ttg gac agc ttg cgc acc gtt gtc atc tgg gca ctg			968
	Thr Arg Met Val Leu Asp Ser Leu Arg Thr Val Val Ile Trp Ala Leu			
	295	300	305	
	agc ctg gca ctg ggc tgg gag gcc ttc cat gca ctg cag atc ctt ggc			1016
15	Ser Leu Ala Leu Gly Trp Glu Ala Phe His Ala Leu Gln Ile Leu Gly			
	310	315	320	
	ttc ctc ata ctc ctt ata ggc act gcc ctc tac aat ggg cta cac cgt			1064
	Phe Leu Ile Leu Leu Ile Gly Thr Ala Leu Tyr Asn Gly Leu His Arg			
	325	330	335	
20	ccg ctg ctg ggc cgc ctg tcc agg ggc cgg ccc ctg gca gag gag agc			1112
	Pro Leu Leu Gly Arg Leu Ser Arg Gly Arg Pro Leu Ala Glu Glu Ser			
	340	345	350	
	gag cag gag aga ctg ctg ggt ggc acc cgc act ccc atc aat gat gcc			1160
	Glu Gln Glu Arg Leu Leu Gly Gly Thr Arg Thr Pro Ile Asn Asp Ala			
25	355	360	365	370
	agc tgagggtccc tggagggttc tactgccacc cgggtgctcc ttctccc			1210
	Ser			
	tgagactgag gccacacagg ctggtgggcc ccgaatgcc tatccccaag gcctcaccct			1270
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	agtggcagac ctcagctetc tggacccttc ctacagcact agagctaaat catgaagttg			1450
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92/177

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                                     1           5
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Trp Ala Ala Leu Leu Tyr Phe Tyr Gly Ile Ile Leu Asn Ser Ile Tyr
                10                15                20
15 cag tgc cct gag cac agt caa ctg aca act ctg ggc gtg gat ggg aag      150
   Gln Cys Pro Glu His Ser Gln Leu Thr Thr Leu Gly Val Asp Gly Lys
                25                30                35
gag ttc cca gag gtc cac ttg ggc cag tgg tac ttt atc gca ggg gca      198
Glu Phe Pro Glu Val His Leu Gly Gln Trp Tyr Phe Ile Ala Gly Ala
20                40                45                50
gct ccc acc aag gag gag ttg gca act ttt gac cct gtg gac aac att      246
Ala Pro Thr Lys Glu Glu Leu Ala Thr Phe Asp Pro Val Asp Asn Ile
                55                60                65
gtc ttc aat atg gct gct ggc tct gcc ccg atg cag ctc cac ctt cgt      294
25 Val Phe Asn Met Ala Ala Gly Ser Ala Pro Met Gln Leu His Leu Arg
                70                75                80                85
gct acc atc cgc atg tgagtggaaa gatgggctct gtgtgccccg g      340
Ala Thr Ile Arg Met
                90
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   atgaagactg agctcttttc cagctcatgc ccaggtggaa tcatgctgaa tgagacaggc      460
   cagggttacc agcgcctttct cctctacaat cgctcaccac atcctcccga aaagtgtgtg      520
   gaggaattca agtccctgac ttcctgectg gactccaaag ccttcttatt gactcctagg      580
   aatcaagagg cctgtgagct gtccaataac tgacctgtaa cttcatctaa gtccccagat      640
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733

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tgggtgttcgc ccaccccggg ccgcgtgagt ggggccccac gcagctcccc gcaactccgtg 180

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cactgcgcat gcggagctcc aaattcaaac agctgttttc agaggctgga gggcggggcg 300

actggtagca gctgggggcta ggagaggctt tctctaggag gcggccgctc gggagcc 357

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atg gtg gac cgg ggc cct ctg ctc acc tcg gcc atc atc ttc tac ctg 405

Met Val Asp Arg Gly Pro Leu Leu Thr Ser Ala Ile Ile Phe Tyr Leu

1

5

10

15

gcc atc ggg gcg gcg atc ttc gaa gtg ctg gag gag cca cac tgg aag 453

Ala Ile Gly Ala Ala Ile Phe Glu Val Leu Glu Glu Pro His Trp Lys

25

20

25

30

gag gcc aag aaa aac tactac aca cag aag ctg cat ctg ctc aag gag 501

Glu Ala Lys Lys Asn Tyr Tyr Thr Gln Lys Leu His Leu Leu Lys Glu

35

40

45

ttc ccg tgc ctg ggt cag gag ggc ctg gac aag atc cta gag gtg gta 549

30

Phe Pro Cys Leu Gly Gln Glu Gly Leu Asp Lys Ile Leu Glu Val Val

50

55

60

tct gat gct gca gga cag ggt gtg gcc atc aca ggg aac cag acc ttc 597

Ser Asp Ala Ala Gly Gln Gly Val Ala Ile Thr Gly Asn Gln Thr Phe

65

70

75

80

35

aac aac tgg aac tgg ccc aat gca atg att ttt gca gcg acc gtc att 645

94/177

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	acc acc att gga tat ggc aat gtg gct ccc aag acc ccc gcc ggt cgc	693
	Thr Thr Ile Gly Tyr Gly Asn Val Ala Pro Lys Thr Pro Ala Gly Arg	
5	100 105 110	
	ctc ttc tgt gtt ttc tat ggt ctc ttc ggg gtg ccg ctc tgc ctg acg	741
	Leu Phe Cys Val Phe Tyr Gly Leu Phe Gly Val Pro Leu Cys Leu Thr	
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	tgg atc agt gcc ctg ggc aag ttc ttc ggg gga cgt gcc aag aga cta	789
10	Trp Ile Ser Ala Leu Gly Lys Phe Phe Gly Gly Arg Ala Lys Arg Leu	
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	ggg cag ttc ctt acc aag aga ggt gtg agt ctg cgg aag gcg cag atc	837
	Gly Gln Phe Leu Thr Lys Arg Gly Val Ser Leu Arg Lys Ala Gln Ile	
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	Thr Cys Thr Val Ile Phe Ile Val Trp Gly Val Leu Val His Leu Val	
	165 170 175	
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	Ile Pro Pro Phe Val Phe Met Val Thr Glu Gly Trp Asn Tyr Ile Glu	
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	Tyr Phe Val Glu Leu Trp Ile Tyr Leu Gly Leu Ala Trp Leu Ser Leu	
	225 230 235 240	
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	Phe Val Asn Trp Lys Val Ser Met Phe Val Glu Val His Lys Ala Ile	
	245 250 255	
	aag aag cgg cgg cgg cga cgg aag gag tcc ttt gag agc tcc cca cac	1173
	Lys Lys Arg Arg Arg Arg Arg Lys Glu Ser Phe Glu Ser Ser Pro His	
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	Ile Lys Gln Ile Gly Lys Lys Ala Met Lys Thr Ser Gly Gly Gly Glu	
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10	acg ggc ccg ggc cca ggg ctg ggg cct caa ggc ggt ggg ctc cca gca	1365
	Thr Gly Pro Gly Pro Gly Leu Gly Pro Gln Gly Gly Gly Leu Pro Ala	
	325 330 335	
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	Leu Pro Pro Ser Leu Val Pro Leu Val Val Tyr Ser Lys Asn Arg Val	
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	ccc acc ttg gaa gag gtg tca cag aca ctg agg agc aaa ggc cac gta	1461
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	Ser Pro Ala Pro Glu Val Phe Met Asn Gln Leu Asp Arg Ile Ser Glu	
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	Glu Cys Glu Pro Trp Asp Ala Gln Asp Tyr His Pro Leu Ile Phe Gln	
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	Asp Ala Ser Ile Thr Phe Val Asn Thr Glu Ala Gly Leu Ser Asp Glu	
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	gag acc tcc aag tcc tcg cta gag gac aac ttg gca ggg gag gag agc	1701
	Glu Thr Ser Lys Ser Ser Leu Glu Asp Asn Leu Ala Gly Glu Glu Ser	
	435 440 445	
	ccc cag cag ggg gct gaa gcc aag gcg ccc ctg aac atg ggc gag ttc	1749
35	Pro Gln Gln Gly Ala Glu Ala Lys Ala Pro Leu Asn Met Gly Glu Phe	

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	Val Pro Tyr Glu Gln Leu Met Asn Glu Tyr Asn Lys Ala Asn Ser Pro			
	485	490	495	
	aag ggc aca tgaggcaggg ccggctcccc accccacctt tgatgg			1890
	Lys Gly Thr			
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 Asp Ser Lys Arg Gly Glu Ala Pro Phe Ala Gln Arg Ile Asp Pro Thr
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 45 50 55
 30 gtg acc ggc cta ggc atc ggg gcc ctg gtg ttg gct att tat ggt tac 245
 Val Thr Gly Leu Gly Ile Gly Ala Leu Val Leu Ala Ile Tyr Gly Tyr
 60 65 70
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 Thr Phe Tyr Ser Ile Ser Gln Glu Arg Phe Leu Asp Glu Leu Glu Asp
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	Leu Ser Pro Leu Ala Ser Ile Thr Gly Ile Ser Leu Phe Leu Ile Ile	
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 Ile Lys Gln Lys Leu Glu Gly Arg Pro Glu Thr Glu Tyr Arg Lys Ala
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 Gln Thr Phe Ser Gly His Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr
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 Arg Ser Val Pro Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser
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 Pro Glu
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100/177

<213> Homo sapience

<400> 91

Met Ala Pro Gln Asn Leu Ser Thr Phe Cys Leu Leu Leu Leu Tyr Leu
 5 1 5 10 15
 Ile Gly Ala Val Ile Ala Gly Arg Asp Phe Tyr Lys Ile Leu Gly Val
 20 25 30
 Pro Arg Ser Ala Ser Ile Lys Asp Ile Lys Lys Ala Tyr Arg Lys Leu
 35 40 45
 10 Ala Leu Gln Leu His Pro Asp Arg Asn Pro Asp Asp Pro Gln Ala Gln
 50 55 60
 Glu Lys Phe Gln Asp Leu Gly Ala Ala Tyr Glu Val Leu Ser Asp Ser
 65 70 75 80
 Glu Lys Arg Lys Gln Tyr Asp Thr Tyr Gly Glu Glu Gly Leu Lys Asp
 15 85 90 95
 Gly His Gln Ser Ser His Gly Asp Ile Phe Ser His Phe Phe Gly Asp
 100 105 110
 Phe Gly Phe Met Phe Gly Gly Thr Pro Arg Gln Gln Asp Arg Asn Ile
 115 120 125
 20 Pro Arg Gly Ser Asp Ile Ile Val Asp Leu Glu Val Thr Leu Glu Glu
 130 135 140
 Val Tyr Ala Gly Asn Phe Val Glu Val Val Arg Asn Lys Pro Val Ala
 145 150 155 160
 Arg Gln Ala Pro Gly Lys Arg Lys Cys Asn Cys Arg Gln Glu Met Arg
 25 165 170 175
 Thr Thr Gln Leu Gly Pro Gly Arg Phe Gln Met Thr Gln Glu Val Val
 180 185 190
 Cys Asp Glu Cys Pro Asn Val Lys Leu Val Asn Glu Glu Arg Thr Leu
 195 200 205
 30 Glu Val Glu Ile Glu Pro Gly Val Arg Asp Gly Met Glu Tyr Pro Phe
 210 215 220
 Ile Gly Glu Gly Glu Pro His Val Asp Gly Glu Pro Gly Asp Leu Arg
 225 230 235 240
 Phe Arg Ile Lys Val Val Lys His Pro Ile Phe Glu Arg Arg Gly Asp
 35 245 250 255

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Asp Leu Tyr Thr Asn Val Thr Ile Ser Leu Val Glu Ser Leu Val Gly
 260 265 270
 Phe Glu Met Asp Ile Thr His Leu Asp Gly His Lys Val His Ile Ser
 275 280 285
 5 Arg Asp Lys Ile Thr Arg Pro Gly Ala Lys Leu Trp Lys Lys Gly Glu
 290 295 300
 Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys Gly Ser Leu Ile Ile
 305 310 315 320
 Thr Phe Asp Val Asp Phe Pro Lys Glu Gln Leu Thr Glu Glu Ala Arg
 10 325 330 335
 Glu Gly Ile Lys Gln Leu Leu Lys Gln Gly Ser Val Gln Lys Val Tyr
 340 345 350
 Asn Gly Leu Gln Gly Tyr
 355
 15
 <210> 92
 <211> 226
 <212> PRT
 <213> Homo sapience
 20
 <400> 92
 Met Lys Met Val Ala Pro Trp Thr Arg Phe Tyr Ser Asn Ser Cys Cys
 1 5 10 15
 Leu Cys Cys His Val Arg Thr Gly Thr Ile Leu Leu Gly Val Trp Tyr
 25 20 25 30
 Leu Ile Ile Asn Ala Val Val Leu Leu Ile Leu Leu Ser Ala Leu Ala
 35 40 45
 Asp Pro Asp Gln Tyr Asn Phe Ser Ser Ser Glu Leu Gly Gly Asp Phe
 50 55 60
 30 Glu Phe Met Asp Asp Ala Asn Met Cys Ile Ala Ile Ala Ile Ser Leu
 65 70 75 80
 Leu Met Ile Leu Ile Cys Ala Met Ala Thr Tyr Gly Ala Tyr Lys Gln
 85 90 95
 Arg Ala Ala Trp Ile Ile Pro Phe Phe Cys Tyr Gln Ile Phe Asp Phe
 35 100 105 110

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Ala Leu Asn Met Leu Val Ala Ile Thr Val Leu Ile Tyr Pro Asn Ser
115 120 125
Ile Gln Glu Tyr Ile Arg Gln Leu Pro Pro Asn Phe Pro Tyr Arg Asp
130 135 140
5 Asp Val Met Ser Val Asn Pro Thr Cys Leu Val Leu Ile Ile Leu Leu
145 150 155 160
Phe Ile Ser Ile Ile Leu Thr Phe Lys Gly Tyr Leu Ile Ser Cys Val
165 170 175
Trp Asn Cys Tyr Arg Tyr Ile Asn Gly Arg Asn Ser Ser Asp Val Leu
10 180 185 190
Val Tyr Val Thr Ser Asn Asp Thr Thr Val Leu Leu Pro Pro Tyr Asp
195 200 205
Asp Ala Thr Val Asn Gly Ala Ala Lys Glu Pro Pro Pro Pro Tyr Val
210 215 220
15 Ser Ala
225

<210> 93
<211> 195
20 <212> PRT
<213> Homo sapience

<400> 93
Met Arg Leu Leu Leu Leu Leu Val Ala Ala Ser Ala Met Val Arg
25 1 5 10 15
Ser Glu Ala Ser Ala Asn Leu Gly Gly Val Pro Ser Lys Arg Leu Lys
20 25 30
Met Gln Tyr Ala Thr Gly Pro Leu Leu Lys Phe Gln Ile Cys Val Ser
35 40 45
30 Xaa Gly Tyr Arg Arg Val Phe Glu Glu Tyr Met Arg Val Ile Ser Gln
50 55 60
Arg Tyr Pro Asp Ile Arg Ile Glu Gly Glu Asn Tyr Leu Pro Gln Pro
65 70 75 80
Ile Tyr Arg His Ile Ala Ser Phe Leu Ser Val Phe Lys Leu Val Leu
35 85 90 95

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Ile Gly Leu Ile Ile Val Gly Lys Asp Pro Phe Ala Phe Phe Gly Met
 100 105 110
 Gln Ala Pro Ser Ile Trp Gln Trp Gly Gln Glu Asn Lys Val Tyr Ala
 115 120 125
 5 Cys Met Met Val Phe Phe Leu Ser Asn Met Ile Glu Asn Gln Cys Met
 130 135 140
 Ser Thr Gly Ala Phe Glu Ile Thr Leu Asn Asp Val Pro Val Trp Ser
 145 150 155 160
 Lys Leu Glu Ser Gly His Leu Pro Ser Met Gln Gln Leu Val Gln Ile
 10 165 170 175
 Leu Asp Asn Glu Met Lys Leu Asn Val His Met Asp Ser Ile Pro His
 180 185 190
 His Arg Ser
 195
 15
 <210> 94
 <211> 339
 <212> PRT
 <213> Homo sapience
 20
 <400> 94
 Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu
 1 5 10 15
 Leu Leu Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu
 25 20 25 30
 Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu
 35 40 45
 Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu
 50 55 60
 30 Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
 65 70 75 80
 Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu
 85 90 95
 Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu
 35 100 105 110

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Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val Leu Gln Glu
115 120 125
Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly Met Ser Gln Arg
130 135 140
5 Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr Arg Lys Leu Ile Glu
145 150 155 160
Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His
165 170 175
Met Ile Glu Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Leu
10 180 185 190
Gly Ile Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Lys His
195 200 205
Ala Leu Arg Gly Phe Phe Asn Gly Leu Arg Thr Glu Leu Ala Thr Tyr
210 215 220
15 Pro Gly Ile Ile Val Ser Asn Ile Cys Pro Gly Pro Val Gln Ser Asn
225 230 235 240
Ile Val Glu Asn Ser Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn
245 250 255
Asn Gly Asp Gln Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu
20 260 265 270
Met Leu Ile Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu
275 280 285
Gln Pro Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp
290 295 300
25 Ala Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe
305 310 315 320
Lys Ser Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys Thr
325 330 335
Lys His Asp
30
<210> 95
<211> 487
<212> PRT
<213> Homo sapience
35

<400> 95

	Met	Asp	Gly	Thr	Glu	Thr	Arg	Gln	Arg	Leu	Asp	Ser	Cys	Gly	Lys
	1				5				10					15	
	Pro	Gly	Glu	Leu	Gly	Leu	Pro	His	Pro	Leu	Ser	Thr	Gly	Gly	Leu
5				20				25					30		
	Val	Ala	Ser	Glu	Asp	Gly	Ala	Leu	Arg	Ala	Pro	Glu	Ser	Gln	Ser
		35					40					45			
	Thr	Pro	Lys	Pro	Leu	Glu	Thr	Glu	Pro	Ser	Arg	Glu	Thr	Ala	Trp
	50						55					60			
10	Ile	Gly	Leu	Gln	Val	Thr	Val	Pro	Phe	Met	Phe	Ala	Gly	Leu	Gly
	65				70					75					80
	Ser	Trp	Ala	Gly	Met	Leu	Leu	Asp	Tyr	Phe	Gln	His	Trp	Pro	Val
				85					90					95	
	Val	Glu	Val	Lys	Asp	Leu	Leu	Thr	Leu	Val	Pro	Pro	Leu	Val	Gly
15			100					105					110		
	Lys	Gly	Asn	Leu	Glu	Met	Thr	Leu	Ala	Ser	Arg	Leu	Ser	Thr	Ala
		115					120					125			
	Asn	Thr	Gly	Gln	Ile	Asp	Asp	Pro	Gln	Glu	Gln	His	Arg	Val	Ile
	130					135					140				
20	Ser	Asn	Leu	Ala	Leu	Ile	Gln	Val	Gln	Ala	Thr	Val	Val	Gly	Leu
	145				150					155					160
	Ala	Ala	Val	Ala	Ala	Leu	Leu	Leu	Gly	Val	Val	Ser	Arg	Glu	Glu
				165					170					175	
	Asp	Val	Ala	Lys	Val	Glu	Leu	Leu	Cys	Ala	Ser	Ser	Val	Leu	Thr
25			180						185				190		
	Phe	Leu	Ala	Ala	Phe	Ala	Leu	Gly	Val	Leu	Met	Val	Cys	Ile	Val
		195					200					205			
	Gly	Ala	Arg	Lys	Leu	Gly	Val	Asn	Pro	Asp	Asn	Ile	Ala	Thr	Pro
	210					215						220			
30	Ala	Ala	Ser	Leu	Gly	Asp	Leu	Ile	Thr	Leu	Ser	Ile	Leu	Ala	Leu
	225				230					235					240
	Ser	Ser	Phe	Phe	Tyr	Arg	His	Lys	Asp	Ser	Arg	Tyr	Leu	Thr	Pro
				245					250				255		
	Val	Cys	Leu	Ser	Phe	Ala	Ala	Leu	Thr	Pro	Val	Trp	Val	Leu	Ile
35			260						265				270		

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Lys Gln Ser Pro Pro Ile Val Lys Ile Leu Lys Phe Gly Trp Phe Pro
 275 280 285
 Ile Ile Leu Ala Met Val Ile Ser Ser Phe Gly Gly Leu Ile Leu Ser
 290 295 300
 5 Lys Thr Val Ser Lys Gln Gln Tyr Lys Gly Met Ala Ile Phe Thr Pro
 305 310 315 320
 Val Ile Cys Gly Val Gly Gly Asn Leu Val Ala Ile Gln Thr Ser Arg
 325 330 335
 Ile Ser Thr Tyr Leu His Met Trp Ser Ala Pro Gly Val Leu Pro Leu
 10 340 345 350
 Gln Met Lys Lys Phe Trp Pro Asn Pro Cys Ser Thr Phe Cys Thr Ser
 355 360 365
 Glu Ile Asn Ser Met Ser Ala Arg Val Leu Leu Leu Leu Val Val Pro
 370 375 380
 15 Gly His Leu Ile Phe Phe Tyr Ile Ile Tyr Leu Val Glu Gly Gln Ser
 385 390 395 400
 Val Ile Asn Ser Gln Thr Phe Val Val Leu Tyr Leu Leu Ala Gly Leu
 405 410 415
 Ile Gln Val Thr Ile Leu Leu Tyr Leu Ala Glu Val Met Val Arg Leu
 20 420 425 430
 Thr Trp His Gln Ala Leu Asp Pro Asp Asn His Cys Ile Pro Tyr Leu
 435 440 445
 Thr Gly Leu Gly Asp Leu Leu Gly Thr Gly Leu Leu Ala Leu Cys Phe
 450 455 460
 25 Phe Thr Asp Trp Leu Leu Lys Ser Lys Ala Glu Leu Gly Gly Ile Ser
 465 470 475 480
 Glu Leu Ala Ser Gly Pro Pro
 485
 30 <210> 96
 <211> 393
 <212> PRT
 <213> Homo sapience
 35 <400> 96

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Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
 1 5 10 15
 Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys
 20 25 30
 5 Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg
 35 40 45
 Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His
 50 55 60
 Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp
 10 65 70 75 80
 Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr
 85 90 95
 Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln
 100 105 110
 15 Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp
 115 120 125
 Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu
 130 135 140
 His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe
 145 150 155 160
 20 Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr
 165 170 175
 Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu
 180 185 190
 25 Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His Met
 195 200 205
 Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala Leu
 210 215 220
 Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly Met
 225 230 235 240
 30 Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly Phe
 245 250 255
 Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro Asn
 260 265 270
 35 Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro Lys

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	275	280	285
	Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr Gly Met		
	290	295	300
5	Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly Ala Arg		
	305	310	315 320
	Tyr Ile Gln Thr Leu Lys Asp His Arg Pro Arg Met Val Trp Asp Ser		
	325	330	335
	Gln Ala Ser Glu His Phe Phe Glu Tyr Lys Lys Ser Arg Ser Gly Arg		
	340	345	350
10	His Val Val Phe Tyr Pro Thr Leu Lys Ser Leu Gln Val Arg Leu Glu		
	355	360	365
	Leu Ala Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Gly Gln		
	370	375	380
	Gly Leu Asp Tyr Phe Tyr Asp Leu Leu		
15	385	390	
	<210> 97		
	<211> 196		
	<212> PRT		
20	<213> Homo sapience		
	<400> 97		
	Met Trp Arg Val Pro Gly Thr Thr Arg Arg Pro Val Thr Gly Glu Ser		
	1	5	10 15
25	Pro Gly Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala		
	20	25	30
	Leu Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly		
	35	40	45
	Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr Gly		
30	50	55	60
	Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln Val Lys		
	65	70	75 80
	Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly Gly Asn Thr		
	85	90	95
35	Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr Lys Val Phe Val		

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100 105 110
 Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met Tyr Thr Ser Lys Asp
 115 120 125
 Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly Gln Ile Ser Ser Ala Tyr
 5 130 135 140
 Pro Ser Gln Glu Gly Gln Val Leu Val Gly Ile Tyr Gly Gln Tyr Gln
 145 150 155 160
 Leu Leu Gly Ile Lys Ser Ile Gly Phe Glu Trp Asn Tyr Pro Leu Glu
 165 170 175
 10 Glu Pro Thr Thr Glu Pro Pro Val Asn Leu Thr Tyr Ser Ala Asn Ser
 180 185 190
 Pro Val Gly Arg
 195
 15 <210> 98
 <211> 107
 <212> PRT
 <213> Homo sapience
 20 <400> 98
 Met Glu Gln Lys Leu Val Glu Glu Ile Leu Gln Ala Ile Thr Met Ser
 1 5 10 15
 Thr Asp Thr Gly Val Ser Leu Pro Ser Tyr Glu Glu Asp Gln Gly Ser
 20 25 30
 25 Lys Leu Ile Arg Lys Ala Lys Glu Ala Pro Phe Val Pro Val Gly Ile
 35 40 45
 Ala Gly Phe Ala Ala Ile Val Ala Tyr Gly Leu Tyr Lys Leu Lys Ser
 50 55 60
 Arg Gly Asn Thr Lys Met Ser Ile His Leu Ile His Met Arg Val Ala
 30 65 70 75 80
 Ala Glu Gly Phe Val Val Gly Ala Met Thr Val Gly Met Gly Tyr Ser
 85 90 95
 Met Tyr Arg Glu Phe Trp Ala Lys Pro Lys Pro
 100 105
 35

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<210> 99

<211> 350

<212> PRT

<213> Homo sapience

5

<400> 99

Met Ser Glu Val Lys Ser Arg Lys Lys Ser Gly Pro Lys Gly Ala Pro

1 5 10 15

Ala Ala Glu Pro Gly Lys Arg Ser Glu Gly Gly Lys Thr Pro Val Ala

10 20 25 30

Arg Ser Ser Gly Gly Gly Gly Trp Ala Asp Pro Arg Thr Cys Leu Ser

35 40 45

Leu Leu Ser Leu Gly Thr Cys Leu Gly Leu Ala Trp Phe Val Phe Gln

50 55 60

15 Gln Ser Glu Lys Phe Ala Lys Val Glu Asn Gln Tyr Gln Leu Leu Lys

65 70 75 80

Leu Glu Thr Asn Glu Phe Gln Gln Leu Gln Ser Lys Ile Ser Leu Ile

85 90 95

Ser Glu Lys Trp Gln Lys Ser Glu Ala Ile Met Glu Gln Leu Lys Ser

20 100 105 110

Phe Gln Ile Ile Ala His Leu Lys Arg Leu Gln Glu Glu Ile Asn Glu

115 120 125

Val Lys Thr Trp Ser Asn Arg Ile Thr Glu Lys Gln Asp Ile Leu Asn

130 135 140

25 Asn Ser Leu Thr Thr Leu Ser Gln Asp Ile Thr Lys Val Asp Gln Ser

145 150 155 160

Thr Thr Ser Met Ala Lys Asp Val Gly Leu Lys Ile Thr Ser Val Lys

165 170 175

Thr Asp Ile Arg Arg Ile Ser Gly Leu Val Thr Asp Val Ile Ser Leu

30 180 185 190

Thr Asp Ser Val Gln Glu Leu Glu Asn Lys Ile Glu Lys Val Glu Lys

195 200 205

Asn Thr Val Lys Asn Ile Gly Asp Leu Leu Ser Ser Ser Ile Asp Arg

210 215 220

35 Thr Ala Thr Leu Arg Lys Thr Ala Ser Glu Asn Ser Gln Arg Ile Asn

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225 230 235 240
 Ser Val Lys Lys Thr Leu Thr Glu Leu Lys Ser Asp Phe Asp Lys His
 245 250 255
 Thr Asp Arg Phe Leu Ser Leu Glu Gly Asp Arg Ala Lys Val Leu Lys
 5 260 265 270
 Thr Val Thr Phe Ala Asn Asp Leu Lys Pro Lys Val Tyr Asn Leu Lys
 275 280 285
 Lys Asp Phe Ser Arg Leu Glu Pro Leu Val Asn Asp Leu Thr Leu Arg
 290 295 300
 10 Ile Gly Arg Leu Val Thr Asp Leu Leu Gln Arg Glu Lys Glu Ile Ala
 305 310 315 320
 Phe Leu Ser Glu Lys Ile Ser Asn Leu Thr Ile Val Gln Ala Glu Ile
 325 330 335
 Lys Asp Ile Lys Asp Glu Ile Ala His Ile Ser Asp Met Asn
 15 340 345 350

 <210> 100
 <211> 107
 <212> PRT
 20 <213> Homo sapience

 <400> 100
 Met Ser Ser Ala Gly Thr Ala Thr Pro Leu Glu Met Asp His Lys Leu
 1 5 10 15
 25 Thr Ser Gln Pro Gly Arg Pro Ser Phe Tyr Cys Asn Ser Arg His Ser
 20 25 30
 Ile Val Gly Ser Ser His Gln Leu Gly Phe Trp Phe Ser His Leu Glu
 35 40 45
 Ser Ser Gly Leu Lys Val Phe Gln Val Ser Leu Pro Cys Glu Cys Val
 30 50 55 60
 Asn Leu Pro Thr Arg Ile Ala Ser Val Val Leu Ser Leu Met Ser Leu
 65 70 75 80
 Leu Val Val Gly Gln Ala Pro Ala Trp Glu Gly Ser Leu Leu Arg Gly
 85 90 95
 35 Arg Pro Ala Gly Gly Ala His Leu Cys Ala Ala

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100

105

<210> 101

<211> 1074

5

<212> DNA

<213> Homo Sapience

<400> 101

	atggctccgc agaacctgag caccttttgc ctggtgctgc tataacctcat cggggcggtg	60
10	attgccggac gagattttota taagatcttg ggggtgcttc gaagtgcctc tataaaggat	120
	attaaaaagg cctataggaa actagccctg cagcttcctc ccgaccggaa ccctgatgat	180
	ccacaagccc aggagaaatt ccaggatctg ggtgctgctt atgaggttct gtcagatagt	240
	gagaaacgga aacagtacga tactttatggt gaagaaggat taaaagatgg tcatcagagc	300
	tcccatggag acatTTTTTt acacttcttt ggggattttg gtttcatgtt tggaggaaacc	360
15	cctcgctcagc aagacagaaa tattccaaga ggaagtgata ttattgtaga tctagaagtc	420
	acttttgaag aagtatatgc aggaaatttt gtggaagtag ttagaaacaa acctgtggca	480
	aggcaggctc ctggcaaacg gaagtgcaat tgtcggcaag agatgcggac caccagctg	540
	ggccctgggc gcttccaaat gaccaggag gtggtctgctg acgaatgccc taatgtcaaa	600
	ctagtgaatg aagaacgaac gctggaagta gaaatagagc ctgggggtgag agacggcatg	660
20	gagtaccctt ttattggaga aggtgagcct cacgtggatg gggagcctgg agatttacgg	720
	ttccgaatca aagttgtcaa gcacccaata tttgaaagga gaggagatga tttgtacaca	780
	aatgtgacaa tctcattagt tgagtcactg gttggctttg agatggatat tactcacttg	840
	gatggtcaca aggtacatat ttccgggat aagatcacca ggccaggagc gaagctatgg	900
	aagaaagggg aagggtctcc caactttgac aacaacaata tcaagggtc tttgataatc	960
25	acttttgatg tggattttcc aaaagaacag ttaacagagg aagcgagaga aggtatcaaa	1020
	cagctactga aacaagggtc agtcagaag gtatacaatg gactgcaagg atat	1074

<210> 102

<211> 678

30

<212> DNA

<213> Homo Sapience

<400> 102

	atgaagatgg tcgcgccttg gacgcggttc tactccaaca gctgctgctt gtgetgcoat	60
35	gtccgcaccg gcaccatcct gctcggcgtc tggatatctga tcatcaatgc tgtggtactg	120

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5 ttgattttat tgagtgcct ggctgaccc gatcagtata acttttcaag ttctgaactg 180
 ggaggtgact ttgagttcat ggatgatgcc aacatgtgca ttgccattgc gattttctctt 240
 ctcatgatcc tgatatgtgc tatggctact taaggagcgt acaagcaacg cgcagcctgg 300
 atcatcccat tcttctgtta ccagatcttt gactttgccc tgaacatgtt ggttgcaatc 360
 actgtgetta tttatccaaa ctccattcag gaatacatat ggcaactgcc tcctaatttt 420
 ccctacagag atgatgtcat gtcagtgaat cctacctgtt tggtccttat tattcttctg 480
 tttattagca ttatcttgac ttttaagggt tacttgatta gctgtgtttg gaactgctac 540
 cgatacatca atggtaggaa ctctctgat gtccctggtt atgttaccag caatgacact 600
 acggtgctgc taccctcgta tgatgatgcc actgtgaatg gtgctgccaa ggagccaccg 660
 10 ccaccttaacg tgtctgcc 678

<210> 103

<211> 585

<212> DNA

15 <213> Homo Sapience

<400> 103

20 atgaggettc tgetgettct cctagtggcg gcgtctgcga tggcccgag cgaggcctcg 60
 gccaatctgg gcggcgtgcc cagcaagaga ttaaagatgc agtacgccac ggggccgctg 120
 ctcaagttcc agatttgtgt ttcttgaggt tataggcggg tgtttgagga gtacatgcgg 180
 gttattagcc agcggtagcc agacatccgc attgaaggag agaattacct cctcaacca 240
 atatatagac acatagcatc ttctctgtca gtcttcaaac tagtattaat aggettaata 300
 attgttggca aggatccttt tgctttcttt ggcatgcaag ctcttagcat ctggcagtgg 360
 ggccaagaaa ataaggttta tgcattgtat atggttttct tcttgagcaa catgattgag 420
 25 aaccagtgtg tgtcaacagg tgcatttgag ataacttta atgatgtacc tgtgtggtct 480
 aagctggaat ctggtcacct tccatccatg caacaacttg ttcaaattct tgacaatgaa 540
 atgaagetca atgtgcatat ggattcaatc ccacaccatc gatca 585

<210> 104

30 <211> 1017

<212> DNA

<213> Homo Sapience

<400> 104

35 atgaactggg agctgctgct gtggctgctg gtgctgtgcg cgtgctcct gctcttggtg 60

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5 cagctgctgc gcttcctgag ggctgacggc gacctgacgc tactatgggc cgagtggcag 120
 ggacgacgcc cagaatggga gctgactgat atgggtgggt gggtgactgg agcctcgagt 180
 ggaattgggtg aggagctggc ttaccagttg tctaaactag gagtttctct tgtgctgtca 240
 gccagaagag tgcattgagct ggaaaggggtg aaaagaagat gcctagagaa tggcaattta 300
 aaagaaaaag atatacttgt tttgcccctt gacctgaccg aacttggttc ccatgaagcg 360
 gctaccaaag ctgttctcca ggagtttggg agaactgaca ttctgggtcaa caatgggtga 420
 atgtcccagc gttctctgtg catggatacc agcttggtatg tctacagaaa gctaatagag 480
 cttaactact tagggacggg gtccttgaca aaatgtgttc tgctcacat gatcgagagg 540
 aagcaaggaa agattgttac tgtgaatagc atcctgggta tcatatctgt acctctttcc 600
 10 attggatact gtgctagcaa gcatgctctc cgggggtttt ttaatggcct tcgaacagaa 660
 cttgccacat acccagggtat aatagtttct aacatttgcc caggacctgt gcaatcaaata 720
 attgtggaga attccctagc tggagaagtc acaaagacta taggcaataa tggagaccag 780
 tcccacaaga tgacaaccag tcgttggtgt cggctgatgt taatcagcat ggccaatgat 840
 ttgaaagaag tttggatctc agaacaacct ttcttgtagg taacatattt gtggcaatac 900
 15 atgccaacct gggcctgggt gataaccaac aagatgggga agaaaaggat tgagaacttt 960
 aagagtgggtg tggatgcaga ctcttcttat tttaaaatct ttaagacaaa acatgac 1017

<210> 105

<211> 1461

20 <212> DNA

<213> Homo Sapiens

<400> 105

25 atggatggga cagagacccg gcagcggagg ctggacagct gtggcaagcc aggggagctg 60
 gggcttcctc accccctcag cacaggagga ctccctgtag cctcagaaga tggagctctc 120
 agggcccctg agagccaaaag cgtgaccccc aagccactgg agactgagcc tagcagggag 180
 accgcctggg ccataggcct tcaggtgacc gtgcccttca tgtttgcagg cctgggactg 240
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 gtgctgatgg tctgtatagt gattgggtgt cgaaagctcg gggtaacccc agacaacatt 660
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	ccgtgttcta ctttctgcac gtcagaaatc aattccatgt cagctcgagt cctgctcttg	1140
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	gtcataaaca gccagacctt tgtggtgctc tacctgctgg caggcctgat ccaggtgaca	1260
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	gccaaaggcc tgcacatagt gcctcggtc ctgtttgagg actggactta cgatgatttc	480
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	ctgctggccc tcctggteat cccgcctgcc atcacccccg ggaccgacca gctgggcatg	720
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	cttgagact cctgggacgt gaaactggga gccttaggtg ggaataccca ggaagtcacc	300
	ctgcagccag gcgaatacat cacaaaagtc tttgtgcct tccaagcttt cctccgggggt	360
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	ctccttggca tcaagagcat tggctttgaa tggaattatc cactagagga gccgacct	540
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	gcaccattcg taccctgttg aatagcgggt tttgcagcaa ttgttgcata tggattatat	180
	aaactgaaga gcaggggaaa tactaaaatg tccattcatt tgatccacat gcgtgtggca	240
	gcccagggct ttgtttagg agcaatgact gttggtatgg gctattccat gtatcgggaa	300
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<210> 109

<211> 1050

<212> DNA

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	ctagaaacca atgaattcca acaacttcaa agtaaaatca gtttaatttc agaaaagtgg	300
	cagaaatctg aagctatcat ggaacaattg aagtcttttc aaataattgc tcactataag	360
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	cggatttcag gtttagtaac tgatgtaata tcattgacag attctgtgca agaactagaa	600
	aataaaatag agaaagtaga aaaaaataca gtaaaaaata taggtgatct tctttcaagc	660
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20	tctgttaaga agacgctaac cgaactaaag agtgacttcg acaaacatac agatagattt	780
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	aaaccaaaagg tgtataatct aaagaaggac ttttcccggt tagaaccatt agtaaattgat	900
	ttaacactac gcattgggag attggttacc gacttactac aaagagagaa agaaattgct	960
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<211> 321

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   gaggagtgtg tggaacagga cccgggacag aggaacc atg gct ccg cag aac ctg      175
                                   Met Ala Pro Gln Asn Leu
                                   1             5
   agc acc ttt tgc ctg ttg ctg cta tac ctc atc ggg gcg gtg att gcc      223
20 Ser Thr Phe Cys Leu Leu Leu Leu Tyr Leu Ile Gly Ala Val Ile Ala
   10             15             20
   gga cga gat ttc tat aag atc ttg ggg gtg cct cga agt gcc tct ata      271
   Gly Arg Asp Phe Tyr Lys Ile Leu Gly Val Pro Arg Ser Ala Ser Ile
   25             30             35
25 aag gat att aaa aag gcc tat agg aaa cta gcc ctg cag ctt cat ccc      319
   Lys Asp Ile Lys Lys Ala Tyr Arg Lys Leu Ala Leu Gln Leu His Pro
   40             45             50
   gac cgg aac cct gat gat cca caa gcc cag gag aaa ttc cag gat ctg      367
   Asp Arg Asn Pro Asp Asp Pro Gln Ala Gln Glu Lys Phe Gln Asp Leu
30 55             60             65             70
   ggt gct gct tat gag gtt ctg tca gat agt gag aaa cgg aaa cag tac      415
   Gly Ala Ala Tyr Glu Val Leu Ser Asp Ser Glu Lys Arg Lys Gln Tyr
   75             80             85
   gat act tat ggt gaa gaa gga tta aaa gat ggt cat cag agc tcc cat      463
35 Asp Thr Tyr Gly Glu Glu Gly Leu Lys Asp Gly His Gln Ser Ser His

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	gga gac att ttt tca cac ttc ttt ggg gat ttt ggt ttc atg ttt gga			511
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	Gly Thr Pro Arg Gln Gln Asp Arg Asn Ile Pro Arg Gly Ser Asp Ile			
	120	125	130	
	att gta gat cta gaa gtc act ttg gaa gaa gta tat gca gga aat ttt			607
	Ile Val Asp Leu Glu Val Thr Leu Glu Glu Val Tyr Ala Gly Asn Phe			
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	gtg gaa gta gtt aga aac aaa cct gtg gca agg cag gct cct ggc aaa			655
	Val Glu Val Val Arg Asn Lys Pro Val Ala Arg Gln Ala Pro Gly Lys			
	155	160	165	
	cgg aag tgc aat tgt cgg caa gag atg cgg acc acc cag ctg ggc cct			703
15	Arg Lys Cys Asn Cys Arg Gln Glu Met Arg Thr Thr Gln Leu Gly Pro			
	170	175	180	
	ggg cgc ttc caa atg acc cag gag gtg gtc tgc gac gaa tgc cct aat			751
	Gly Arg Phe Gln Met Thr Gln Glu Val Val Cys Asp Glu Cys Pro Asn			
	185	190	195	
20	gtc aaa cta gtg aat gaa gaa cga acg ctg gaa gta gaa ata gag cct			799
	Val Lys Leu Val Asn Glu Glu Arg Thr Leu Glu Val Glu Ile Glu Pro			
	200	205	210	
	ggg gtg aga gac ggc atg gag tac ccc ttt att gga gaa ggt gag cct			847
	Gly Val Arg Asp Gly Met Glu Tyr Pro Phe Ile Gly Glu Gly Glu Pro			
25	215	220	225	230
	cac gtg gat ggg gag cct gga gat tta cgg ttc cga atc aaa gtt gtc			895
	His Val Asp Gly Glu Pro Gly Asp Leu Arg Phe Arg Ile Lys Val Val			
	235	240	245	
	aag cac cca ata ttt gaa agg aga gga gat gat ttg tac aca aat gtg			943
30	Lys His Pro Ile Phe Glu Arg Arg Gly Asp Asp Leu Tyr Thr Asn Val			
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	aca atc tca tta gtt gag tca ctg gtt ggc ttt gag atg gat att act			991
	Thr Ile Ser Leu Val Glu Ser Leu Val Gly Phe Glu Met Asp Ile Thr			
	265	270	275	
35	cac ttg gat ggt cac aag gta cat att tcc cgg gat aag atc acc agg			1039

	His Leu Asp Gly His Lys Val His Ile Ser Arg Asp Lys Ile Thr Arg	
	280	285
	cca gga gcg aag cta tgg aag aaa ggg gaa ggg ctc ccc aac ttt gac	1087
	Pro Gly Ala Lys Leu Trp Lys Lys Gly Glu Gly Leu Pro Asn Phe Asp	
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	Asn Asn Asn Ile Lys Gly Ser Leu Ile Ile Thr Phe Asp Val Asp Phe	
	315	320
	cca aaa gaa cag tta aca gag gaa gcg aga gaa ggt atc aaa cag cta	1183
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	330	335
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	Leu Lys Gln Gly Ser Val Gln Lys Val Tyr Asn Gly Leu Gln Gly Tyr	
	345	350
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	gcgggcgcac gggcgagcgg gccgggagcc ggagcggcgg aggagccggc agcagcggcg	180
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	Gly Val Trp Tyr Leu Ile Ile Asn Ala Val Val Leu Leu Ile Leu Leu	
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	Ser Ala Leu Ala Asp Pro Asp Gln Tyr Asn Phe Ser Ser Ser Glu Leu	
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	Gly Gly Asp Phe Glu Phe Met Asp Asp Ala Asn Met Cys Ile Ala Ile	
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	Ala Ile Ser Leu Leu Met Ile Leu Ile Cys Ala Met Ala Thr Tyr Gly	
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	gcg tac aag caa cgc gca gcc tgg atc atc cca ttc ttc tgt tac cag	577
20	Ala Tyr Lys Gln Arg Ala Ala Trp Ile Ile Pro Phe Phe Cys Tyr Gln	
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	atc ttt gac ttt gcc ctg aac atg ttg gtt gca atc act gtg ctt att	625
	Ile Phe Asp Phe Ala Leu Asn Met Leu Val Ala Ile Thr Val Leu Ile	
	110 115 120	
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	Tyr Pro Asn Ser Ile Gln Glu Tyr Ile Arg Gln Leu Pro Pro Asn Phe	
	125 130 135 140	
	ccc tac aga gat gat gtc atg tca gtg aat cct acc tgt ttg gtc ctt	721
	Pro Tyr Arg Asp Asp Val Met Ser Val Asn Pro Thr Cys Leu Val Leu	
30	145 150 155	
	att att ctt ctg ttt att agc att atc ttg act ttt aag ggt tac ttg	769
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	att agc tgt gtt tgg aac tgc tac cga tac atc aat ggt agg aac tcc	817
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	190	195	200	
5	ccc ccg tat gat gat gcc act gtg aat ggt gct gcc aag gag cca ccg			913
	Pro Pro Tyr Asp Asp Ala Thr Val Asn Gly Ala Ala Lys Glu Pro Pro			
	205	210	215	220
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	Pro Pro Tyr Val Ser Ala			
10	225			
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	Leu Leu Leu Leu Val Ala Ala Ser Ala Met Val Arg Ser Glu Ala Ser	
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	gcc aat ctg ggc ggc gtg ccc agc aag aga tta aag atg cag tac gcc	150
	Ala Asn Leu Gly Gly Val Pro Ser Lys Arg Leu Lys Met Gln Tyr Ala	
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	acg ggg ccg ctg ctc aag ttc cag att tgt gtt tcc tga ggt tat agg	198
15	Thr Gly Pro Leu Leu Lys Phe Gln Ile Cys Val Ser Xaa Gly Tyr Arg	
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	Arg Val Phe Glu Glu Tyr Met Arg Val Ile Ser Gln Arg Tyr Pro Asp	
	55 60 65	
20	atc cgc att gaa gga gag aat tac ctc cct caa cca ata tat aga cac	294
	Ile Arg Ile Glu Gly Glu Asn Tyr Leu Pro Gln Pro Ile Tyr Arg His	
	70 75 80	
	ata gca tct ttc ctg tca gtc ttc aaa cta gta tta ata ggc tta ata	342
	Ile Ala Ser Phe Leu Ser Val Phe Lys Leu Val Leu Ile Gly Leu Ile	
25	85 90 95 100	
	att gtt ggc aag gat cct ttt gct ttc ttt ggc atg caa gct cct agc	390
	Ile Val Gly Lys Asp Pro Phe Ala Phe Phe Gly Met Gln Ala Pro Ser	
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	atc tgg cag tgg ggc caa gaa aat aag gtt tat gca tgt atg atg gtt	438
30	Ile Trp Gln Trp Gly Gln Glu Asn Lys Val Tyr Ala Cys Met Met Val	
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	Phe Phe Leu Ser Asn Met Ile Glu Asn Gln Cys Met Ser Thr Gly Ala	
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	Gly His Leu Pro Ser Met Gln Gln Leu Val Gln Ile Leu Asp Asn Glu	
5	165 170 175 180	
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	Met Lys Leu Asn Val His Met Asp Ser Ile Pro His His Arg Ser	
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	agatgctttc ttggcaggct cgttggtacct cttggaaaac ctcaatgcaa gatagtgttt	800
	cagtgtctggc atatttttga attctgcaca ttcattggagt gcaataatac tgtatagctt	860
	tccccacctc ccacaaaatc acccagttaa tgtgtgtgtg tgtttttttt ttttaaggtaa	920
	acattactac ttgtaacttt ttttcttagt catatttgaa aaagtagaaa attgagttac	980
15	aatttgattt tttttccaaa gatgtctgtt aaatctgttg tgcttttata tgaatatttg	1040
	ttttttatag tttaaaattg atcctttggg aatccagttg aagtcccaa atactttata	1100
	agagtttatc agacatctct aatttggcca tgtccagttt atacagttta caaaatatag	1160
	cagatgcaag attatggggg aaatcctata ttcagagtac tctataaatt tttgtgtatg	1220
	tgtgtatgtg cgtgtgatta ccagagaact actaaaaaaa ccaactgctt tttaaatcct	1280
20	attgtgtagt taaagtgtca tgccttgacc aatctaataa attgattaat taactgggcc	1340
	tttatactta actaaataaa aaactaagca gatatgagtt	1380
	<210> 114	
	<211> 1292	
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	<220>	
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30	<400> 114	
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	gactctgggtg cgggcgctct tcttcccccc gagctggggc tgcgcggccg ca atg aac	118
	Met Asn	
35	1	

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	tgg gag ctg ctg ctg tgg ctg ctg gtg ctg tgc gcg ctg ctc ctg ctc	166
	Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu Leu	
	5 10 15	
5	ttg gtg cag ctg ctg cgc ttc ctg agg gct gac ggc gac ctg acg cta	214
	Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu Thr Leu	
	20 25 30	
	cta tgg gcc gag tgg cag gga cga cgc cca gaa tgg gag ctg act gat	262
	Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu Thr Asp	
	35 40 45 50	
10	atg gtg gtg tgg gtg act gga gcc tcg agt gga att ggt gag gag ctg	310
	Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu Leu	
	55 60 65	
	gct tac cag ttg tct aaa cta gga gtt tct ctt gtg ctg tca gcc aga	358
	Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser Ala Arg	
15	70 75 80	
	aga gtg cat gag ctg gaa agg gtg aaa aga aga tgc cta gag aat ggc	406
	Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu Asn Gly	
	85 90 95	
	aat tta aaa gaa aaa gat ata ctt gtt ttg ccc ctt gac ctg acc gac	454
20	Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu Thr Asp	
	100 105 110	
	act ggt tcc cat gaa gcg gct acc aaa gct gtt ctc cag gag ttt ggt	502
	Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val Leu Gln Glu Phe Gly	
	115 120 125 130	
25	aga atc gac att ctg gtc aac aat ggt gga atg tcc cag cgt tct ctg	550
	Arg Ile Asp Ile Leu Val Asn Asn Gly Gly Met Ser Gln Arg Ser Leu	
	135 140 145	
	tgc atg gat acc agc ttg gat gtc tac aga aag cta ata gag ctt aac	598
	Cys Met Asp Thr Ser Leu Asp Val Tyr Arg Lys Leu Ile Glu Leu Asn	
30	150 155 160	
	tac tta ggg acg gtg tcc ttg aca aaa tgt gtt ctg cct cac atg atc	646
	Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His Met Ile	
	165 170 175	
	gag agg aag caa gga aag att gtt act gtg aat agc atc ctg ggt atc	694
35	Glu Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Leu Gly Ile	

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	180	185	190	
	ata tct gta cct ctt tcc att gga tac tgt gct agc aag cat gct ctc			742
	Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Lys His Ala Leu			
	195	200	205	210
5	cgg ggt ttt ttt aat ggc ctt cga aca gaa ctt gcc aca tac cca ggt			790
	Arg Gly Phe Phe Asn Gly Leu Arg Thr Glu Leu Ala Thr Tyr Pro Gly			
		215	220	225
	ata ata gtt tct aac att tgc cca gga cct gtg caa tca aat att gtg			838
	Ile Ile Val Ser Asn Ile Cys Pro Gly Pro Val Gln Ser Asn Ile Val			
10		230	235	240
	gag aat tcc cta gct gga gaa gtc aca aag act ata ggc aat aat gga			886
	Glu Asn Ser Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn Asn Gly			
		245	250	255
	gac cag tcc cac aag atg aca acc agt cgt tgt gtg cgg ctg atg tta			934
15	Asp Gln Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu Met Leu			
		260	265	270
	atc agc atg gcc aat gat ttg aaa gaa gtt tgg atc tca gaa caa cct			982
	Ile Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu Gln Pro			
		275	280	285
20	ttc ttg tta gta aca tat ttg tgg caa tac atg cca acc tgg gcc tgg			1030
	Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp Ala Trp			
		295	300	305
	tgg ata acc aac aag atg ggg aag aaa agg att gag aac ttt aag agt			1078
	Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe Lys Ser			
25		310	315	320
	ggt gtg gat gca gac tct tct tat ttt aaa atc ttt aag aca aaa cat			1126
	Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys Thr Lys His			
		325	330	335
	gac tgaaaagagc atctgtactt ttcaagccac tggagggaaa aatggaaaac a			1180
30	Asp			
	tgaaaacagc aatctttctta tgctttctgaa taatcaaaga ctaattttgtg gttttacttt			1240
	ttaatagata tgacttttgc tccaacatgg aatgaaataa aaaataagta at			1292
35	<210> 115			

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<211> 2168

<212> DNA

<213> Homo Sapience

<220>

5 <221> CDS

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10	atg gat ggg aca gag acc cgg cag cgg agg ctg gac agc tgt ggc aag	103
	Met Asp Gly Thr Glu Thr Arg Gln Arg Arg Leu Asp Ser Cys Gly Lys	
	1 5 10 15	
	cca ggg gag ctg ggg ctt cct cac ccc ctc agc aca gga gga ctc cct	151
	Pro Gly Glu Leu Gly Leu Pro His Pro Leu Ser Thr Gly Gly Leu Pro	
15	20 25 30	
	gta gcc tca gaa gat gga gct ctc agg gcc cct gag agc caa agc gtg	199
	Val Ala Ser Glu Asp Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val	
	35 40 45	
	acc ccc aag cca ctg gag act gag cct agc agg gag acc gcc tgg tcc	247
20	Thr Pro Lys Pro Leu Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser	
	50 55 60	
	ata ggc ctt cag gtg acc gtg ccc ttc atg ttt gca ggc ctg gga ctg	295
	Ile Gly Leu Gln Val Thr Val Pro Phe Met Phe Ala Gly Leu Gly Leu	
	65 70 75 80	
25	tcc tgg gcc ggc atg ctt ctg gac tat ttc cag cac tgg cct gtg ttt	343
	Ser Trp Ala Gly Met Leu Leu Asp Tyr Phe Gln His Trp Pro Val Phe	
	85 90 95	
	gtg gag gtg aaa gac ctt ttg aca ttg gtg ccg ccc ctg gtg ggc ctg	391
	Val Glu Val Lys Asp Leu Leu Thr Leu Val Pro Pro Leu Val Gly Leu	
30	100 105 110	
	aag ggg aac ctg gag atg aca ctg gca tcc aga ctc tcc aca gct gcc	439
	Lys Gly Asn Leu Glu Met Thr Leu Ala Ser Arg Leu Ser Thr Ala Ala	
	115 120 125	
	aac act gga caa att gat gac ccc cag gag cag cac aga gtc atc agc	487
35	Asn Thr Gly Gln Ile Asp Asp Pro Gln Glu Gln His Arg Val Ile Ser	

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	130	135	140	
	agc aac ctg gcc ctc atc cag gtg cag gcc act gtc gtg ggg ctc ttg			535
	Ser Asn Leu Ala Leu Ile Gln Val Gln Ala Thr Val Val Gly Leu Leu			
	145	150	155	160
5	gct gct gtg gct gcg ctg ctg ttg ggc gtg gtg tct cga gag gaa gtg			583
	Ala Ala Val Ala Ala Leu Leu Leu Gly Val Val Ser Arg Glu Glu Val			
	165	170	175	
	gat gtc gcc aag gtg gag ttg ctg tgt gcc agc agt gtc ctc act gcc			631
	Asp Val Ala Lys Val Glu Leu Leu Cys Ala Ser Ser Val Leu Thr Ala			
10	180	185	190	
	ttc ctt gca gcc ttt gcc ctg ggg gtg ctg atg gtc tgt ata gtg att			679
	Phe Leu Ala Ala Phe Ala Leu Gly Val Leu Met Val Cys Ile Val Ile			
	195	200	205	
	ggg gct cga aag ctc ggg gtc aac cca gac aac att gcc acg ccc att			727
15	Gly Ala Arg Lys Leu Gly Val Asn Pro Asp Asn Ile Ala Thr Pro Ile			
	210	215	220	
	gca gcc agc ctg gga gac ctc atc aca ctg tcc att ctg gct ttg gtt			775
	Ala Ala Ser Leu Gly Asp Leu Ile Thr Leu Ser Ile Leu Ala Leu Val			
	225	230	235	240
20	agc agc ttc ttc tac aga cac aaa gat agt cgg tat ctg acg ccg ctg			823
	Ser Ser Phe Phe Tyr Arg His Lys Asp Ser Arg Tyr Leu Thr Pro Leu			
	245	250	255	
	gtc tgc ctc agc ttt gcg gct ctg acc cca gtg tgg gtc ctc att gcc			871
	Val Cys Leu Ser Phe Ala Ala Leu Thr Pro Val Trp Val Leu Ile Ala			
25	260	265	270	
	aag cag agc cca ccc atc gtg aag atc ctg aag ttt ggc tgg ttc cca			919
	Lys Gln Ser Pro Pro Ile Val Lys Ile Leu Lys Phe Gly Trp Phe Pro			
	275	280	285	
	atc atc ctg gcc atg gtc atc agc agt ttc gga gga ctc atc ttg agc			967
30	Ile Ile Leu Ala Met Val Ile Ser Ser Phe Gly Gly Leu Ile Leu Ser			
	290	295	300	
	aaa acc gtt tct aaa cag cag tac aaa ggc atg gcg ata ttt acc ccc			1015
	Lys Thr Val Ser Lys Gln Gln Tyr Lys Gly Met Ala Ile Phe Thr Pro			
	305	310	315	320
35	gtc ata tgt ggt gtt ggt ggc aat ctg gtg gcc att cag acc agc cga			1063

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	Val Ile Cys Gly Val Gly Gly Asn Leu Val Ala Ile Gln Thr Ser Arg	
	325 330 335	
	atc tca acc tac ctg cac atg tgg agt gca cct ggc gtc ctg ccc ctc	1111
	Ile Ser Thr Tyr Leu His Met Trp Ser Ala Pro Gly Val Leu Pro Leu	
5	340 345 350	
	cag atg aag aaa ttc tgg ccc aac ccg tgt tct act ttc tgc acg tca	1159
	Gln Met Lys Lys Phe Trp Pro Asn Pro Cys Ser Thr Phe Cys Thr Ser	
	355 360 365	
	gaa atc aat tcc atg tca gct cga gtc ctg ctc ttg ctg gtg gtc cca	1207
10	Glu Ile Asn Ser Met Ser Ala Arg Val Leu Leu Leu Leu Val Val Pro	
	370 375 380	
	ggc cat ctg att ttc ttc tac atc atc tac ctg gtg gag ggt cag tca	1255
	Gly His Leu Ile Phe Phe Tyr Ile Ile Tyr Leu Val Glu Gly Gln Ser	
	385 390 395 400	
15	gtc ata aac agc cag acc ttt gtg gtg ctc tac ctg ctg gca ggc ctg	1303
	Val Ile Asn Ser Gln Thr Phe Val Val Leu Tyr Leu Leu Ala Gly Leu	
	405 410 415	
	atc cag gtg aca atc ctg ctg tac ctg gca gaa gtg atg gtt cgg ctg	1351
	Ile Gln Val Thr Ile Leu Leu Tyr Leu Ala Glu Val Met Val Arg Leu	
20	420 425 430	
	act tgg cac cag gcc ctg gat cct gac aac cac tgc atc ccc tac ctt	1399
	Thr Trp His Gln Ala Leu Asp Pro Asp Asn His Cys Ile Pro Tyr Leu	
	435 440 445	
	aca ggg ctg ggg gac ctg ctc ggt act ggc ctc ctg gca ctc tgc ttt	1447
25	Thr Gly Leu Gly Asp Leu Leu Gly Thr Gly Leu Leu Ala Leu Cys Phe	
	450 455 460	
	ttc act gac tgg cta ctg aag agc aag gca gag ctg ggt ggc atc tca	1495
	Phe Thr Asp Trp Leu Leu Lys Ser Lys Ala Glu Leu Gly Gly Ile Ser	
	465 470 475 480	
30	gaa ctg gca tct gga cct ccc taactgggcc ccgctggtcc catttgctca ttag	1550
	Glu Leu Ala Ser Gly Pro Pro	
	485	
	aatttctct cacaatcagt ggatacagaa ttcagtttct cccttgccag gtccttgga	1610
	tgggtgaccc ctgcctctgc agtagccttt tgtgagctct ctaaggtagc tctcacacac	1670
35	ctcggtctct ggggtgatac ctgagcctgc aatagagccc tgaaatcaag agcatggctt	1730

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	gagtgtgtga atatgatgtg tgcacatgct taatgagcgt gcaagtgtgc acacgtttgt	1790
	ggagaggagg gtgttctggc ctgagaagct aaagaagagg catgtccagt atgctttgca	1850
	gggtgtgttt gctctttttcc atgcccacgc aaccacagatt ggggtggagc aggaaggagc	1910
	tcttttctgt tcccaagcct cagaactctt gagctgtggc ttacttgctg tcttcaccag	1970
5	gttcaagctc cgtggggccac actgctgctg tgccaagaag gtgtacagcc tccccaggat	2030
	ggggcctcat acaacccttc atctgcactc aacatttaac cgtgtccttg ctgtcttttt	2090
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20	cctactgtga cacacctacc atg cgg aca ctc ttc aac ctc ctc tgg ctt	110
	Met Arg Thr Leu Phe Asn Leu Leu Trp Leu	
	1 5 10	
	gcc ctg gcc tgc agc cct gtt cac act acc ctg tca aag tca gat gcc	158
	Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala	
25	15 20 25	
	aaa aaa gcc gcc tca aag acg ctg ctg gag aag agt cag ttt tca gat	203
	Lys Lys Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp	
	30 35 40	
	aag ccg gtg caa gac cgg ggt ttg gtg gtg acg gac ctc aaa gct gag	254
30	Lys Pro Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu	
	45 50 55	
	agt gtg gtt ctt gag cat cgc agc tac tgc tgc gca aag gcc cgg gac	302
	Ser Val Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp	
	60 65 70	
35	aga cac ttt gct ggg gat gta ctg ggc tat gtc act cca tgg aac agc	350

	Arg His Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser	
	75	80 85 90
	cat ggc tac gat gtc acc aag gtc ttt ggg agc aag ttc aca cag atc	398
	His Gly Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile	
5	95 100 105	
	tca ccc gtc tgg ctg cag ctg aag aga cgt ggc cgt gag atg ttt gag	446
	Ser Pro Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu	
	110 115 120	
	gtc acg ggc ctc cac gac gtg gac caa ggg tgg atg cga gct gtc agg	494
10	Val Thr Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg	
	125 130 135	
	aag cat gcc aag ggc ctg cac ata gtg cct cgg ctc ctg ttt gag gac	542
	Lys His Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp	
	140 145 150	
15	tgg act tac gat gat ttc cgg aac gtc tta gac agt gag gat gag ata	590
	Trp Thr Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile	
	155 160 165 170	
	gag gag ctg agc aag acc gtg gtc cag gtg gca aag aac cag cat ttc	638
	Glu Glu Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe	
20	175 180 185	
	gat ggc ttc gtg gtg gag gtc tgg aac cag ctg cta agc cag aag cgc	686
	Asp Gly Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg	
	190 195 200	
	gtg ggc ctc atc cac atg ctc acc cac ttg gcc gag gct ctg cac cag	734
25	Val Gly Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln	
	205 210 215	
	gcc cgg ctg ctg gcc ctc ctg gtc atc ccg cct gcc atc acc ccc ggg	782
	Ala Arg Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly	
	220 225 230	
30	acc gac cag ctg ggc atg ttc acg cac aag gag ttt gag cag ctg gcc	830
	Thr Asp Gln Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala	
	235 240 245 250	
	ccc gtg ctg gat ggt ttc agc ctc atg acc tac gac tac tct aca gcg	878
	Pro Val Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala	
35	255 260 265	

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cat cag cct ggc cct aat gca ccc ctg tcc tgg gtt cga gcc tgc gtc 926
 His Gln Pro Gly Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val
 270 275 280
 cag gtc ctg gac ccg aag tcc aag tgg cga agc aaa atc ctc ctg ggg 974
 5 Gln Val Leu Asp Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly
 285 290 295
 ctc aac ttc tat ggt atg gac tac gcg acc tcc aag gat gcc cgt gag 1022
 Leu Asn Phe Tyr Gly Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu
 300 305 310
 cct gtt gtc ggg gcc agg tac atc cag aca ctg aag gac cac agg ccc 1070
 10 Pro Val Val Gly Ala Arg Tyr Ile Gln Thr Leu Lys Asp His Arg Pro
 315 320 325 330
 cgg atg gtg tgg gac agc cag gcc tca gag cac ttc ttc gag tac aag 1118
 Arg Met Val Trp Asp Ser Gln Ala Ser Glu His Phe Phe Glu Tyr Lys
 15 335 340 345
 aag agc cgc agt ggg agg cac gtc gtc ttc tac cca acc ctg aag tcc 1166
 Lys Ser Arg Ser Gly Arg His Val Val Phe Tyr Pro Thr Leu Lys Ser
 350 355 360
 ctg cag gtg cgg ctg gag ctg gcc cgg gag ctg ggc gtt ggg gtc tct 1214
 20 Leu Gln Val Arg Leu Glu Leu Ala Arg Glu Leu Gly Val Gly Val Ser
 365 370 375
 atc tgg gag ctg ggc cag gcc ctg gac tac ttc tac gac ctg ctc t 1260
 Ile Trp Glu Leu Gly Gln Gly Leu Asp Tyr Phe Tyr Asp Leu Leu
 380 385 390
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<220>

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35

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<400> 117

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5	gag agc cct ggg atg cac cgg cca gag gcc atg ctg ctg ctg ctc acg	97
	Glu Ser Pro Gly Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr	
	15 20 25 30	
	ctt gcc ctc ctg ggg ggc ccc acc tgg gca ggg aag atg tat ggc cct	145
	Leu Ala Leu Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro	
10	35 40 45	
	gga gga ggc aag tat ttc agc acc act gaa gac tac gac cat gaa atc	193
	Gly Gly Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile	
	50 55 60	
	aca ggg ctg cgg gtg tct gta ggt ctt ctc ctg gtg aaa agt gtc cag	241
15	Thr Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln	
	65 70 75	
	gtg aaa ctt gga gac tcc tgg gac gtg aaa ctg gga gcc tta ggt ggg	289
	Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly Gly	
	80 85 90	
20	aat acc cag gaa gtc acc ctg cag cca ggc gaa tac atc aca aaa gtc	337
	Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr Lys Val	
	95 100 105 110	
	ttt gtc gcc ttc caa gct ttc ctc cgg ggt atg gtc atg tac acc agc	385
	Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met Tyr Thr Ser	
25	115 120 125	
	aag gac cgc tat ttc tat ttt ggg aag ctt gat ggc cag atc tcc tct	433
	Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly Gln Ile Ser Ser	
	130 135 140	
	gcc tac ccc agc caa gag ggg cag gtg ctg gtg ggc atc tat ggc cag	481
30	Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val Gly Ile Tyr Gly Gln	
	145 150 155	
	tat caa ctc ctt ggc atc aag agc att ggc ttt gaa tgg aat tat cca	529
	Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly Phe Glu Trp Asn Tyr Pro	
	160 165 170	
35	cta gag gag ccg acc act gag cca cca gtt aat ctc aca tac tca gca	577

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Leu Glu Glu Pro Thr Thr Glu Pro Pro Val Asn Leu Thr Tyr Ser Ala
 175 180 185 190
 aac tca ccc gtg ggt cgc taggggtggg tatggggcca tccgagctga ggcca 630
 Asn Ser Pro Val Gly Arg
 5 195
 tctgtgtggt ggtggctgat ggtactggag taactgagtc gggacgctga atctgaatcc 690
 accaataaat aaagcttctg c 711

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 20 atgagggagg agaggtggag ttgccggggc tcaggcccg cctcgagcat gggcggatga 180
 gaggagtcgg gagccgaggc ctagggtcct tcgggtgagg ggagacggag ccagcgagga 240
 g atg gag cag aag ctt gtg gag gag att ctt caa gca atc act atg 286
 Met Glu Gln Lys Leu Val Glu Glu Ile Leu Gln Ala Ile Thr Met
 1 5 10 15
 25 tca aca gac aca ggt gtt tcc ctt cct tca tat gag gaa gat cag gga 334
 Ser Thr Asp Thr Gly Val Ser Leu Pro Ser Tyr Glu Glu Asp Gln Gly
 20 25 30
 tca aaa ctc att cga aaa gct aaa gag gca cca ttc gta ccc gtt gga 382
 Ser Lys Leu Ile Arg Lys Ala Lys Glu Ala Pro Phe Val Pro Val Gly
 30 35 40 45
 ata gcg ggt ttt gca gca att gtt gca tat gga tta tat aaa ctg aag 430
 Ile Ala Gly Phe Ala Ala Ile Val Ala Tyr Gly Leu Tyr Lys Leu Lys
 50 55 60
 agc agg gga aat act aaa atg tcc att cat ctg atc cac atg cgt gtg 478
 35 Ser Arg Gly Asn Thr Lys Met Ser Ile His Leu Ile His Met Arg Val

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	65	70	75	
	gca gcc caa ggc ttt gtt gta gga gca atg act gtt ggt atg ggc tat			526
	Ala Ala Gln Gly Phe Val Val Gly Ala Met Thr Val Gly Met Gly Tyr			
	80	85	90	95
5	tcc atg tat cgg gaa ttc tgg gca aaa cct aag cct tagaagaa			570
	Ser Met Tyr Arg Glu Phe Trp Ala Lys Pro Lys Pro			
	100	105		
	gagatgctgt cttggtcttg ttggaggagc ttgctttagt tagatgtcctt attattaaag			630
	ttacctatta ttgttggaat			651
10				
	<210> 119			
	<211> 1310			
	<212> DNA			
	<213> Homo Sapiens			
15	<220>			
	<221> CDS			
	<222> (78)...(1130)			
	<400> 119			
20	cgaacgccaa ggcggccacg tctgctccc cctggtgaag aagctgccct gggcttgctg			60
	tctagggtc tccagac atg tct gag gtg aag agc cgg aag aag tgc ggg			110
	Met Ser Glu Val Lys Ser Arg Lys Lys Ser Gly			
	1	5	10	
	ccc aag gga gcc cct gct gcg gag ccc ggg aag cgg agc gag ggc ggg			158
25	Pro Lys Gly Ala Pro Ala Ala Glu Pro Gly Lys Arg Ser Glu Gly Gly			
	15	20	25	
	aag acc ccc gtg gcc cgg agc agc gga ggc ggg ggc tgg gca gac ccc			206
	Lys Thr Pro Val Ala Arg Ser Ser Gly Gly Gly Gly Trp Ala Asp Pro			
	30	35	40	
30	cga acg tgc ctg agc ctg ctg tgc ctg ggg acg tgc ctg ggc ctg gcc			254
	Arg Thr Cys Leu Ser Leu Leu Ser Leu Gly Thr Cys Leu Gly Leu Ala			
	45	50	55	
	tgg ttt gta ttt cag cag tca gaa aaa ttt gca aag gtg gaa aac caa			302
	Trp Phe Val Phe Gln Gln Ser Glu Lys Phe Ala Lys Val Glu Asn Gln			
35	60	65	70	75

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	tac cag tta ctg aaa cta gaa acc aat gaa ttc caa caa ctt caa agt	350
	Tyr Gln Leu Leu Lys Leu Glu Thr Asn Glu Phe Gln Gln Leu Gln Ser	
	80 85 90	
	aaa atc agt tta att tca gaa aag tgg cag aaa tct gaa gct atc atg	398
5	Lys Ile Ser Leu Ile Ser Glu Lys Trp Gln Lys Ser Glu Ala Ile Met	
	95 100 105	
	gaa caa ttg aag tct ttt caa ata att gct cat cta aag cgt cta cag	446
	Glu Gln Leu Lys Ser Phe Gln Ile Ile Ala His Leu Lys Arg Leu Gln	
	110 115 120	
10	gaa gaa att aat gag gta aaa act tgg tcc aat agg ata act gaa aaa	494
	Glu Glu Ile Asn Glu Val Lys Thr Trp Ser Asn Arg Ile Thr Glu Lys	
	125 130 135	
	cag gat ata ctg aac aac agt ctg acg acg ctt tct caa gac att aca	542
	Gln Asp Ile Leu Asn Asn Ser Leu Thr Thr Leu Ser Gln Asp Ile Thr	
15	140 145 150 155	
	aaa gta gac caa agt aca act tcc atg gca aaa gat gtt ggt ctc aag	590
	Lys Val Asp Gln Ser Thr Thr Ser Met Ala Lys Asp Val Gly Leu Lys	
	160 165 170	
	att aca agt gta aaa aca gat ata cga cgg att tca ggt tta gta act	638
20	Ile Thr Ser Val Lys Thr Asp Ile Arg Arg Ile Ser Gly Leu Val Thr	
	175 180 185	
	gat gta ata tca ttg aca gat tct gtg caa gaa cta gaa aat aaa ata	686
	Asp Val Ile Ser Leu Thr Asp Ser Val Gln Glu Leu Glu Asn Lys Ile	
	190 195 200	
25	gag aaa gta gaa aaa aat aca gta aaa aat ata ggt gat ctt ctt tca	734
	Glu Lys Val Glu Lys Asn Thr Val Lys Asn Ile Gly Asp Leu Leu Ser	
	205 210 215	
	agc agt att gat cga aca gca acg ctc cga aag aca gca tct gaa aat	782
	Ser Ser Ile Asp Arg Thr Ala Thr Leu Arg Lys Thr Ala Ser Glu Asn	
30	220 225 230 235	
	tca caa aga att aac tct gtt aag aag acg cta acc gaa cta aag agt	830
	Ser Gln Arg Ile Asn Ser Val Lys Lys Thr Leu Thr Glu Leu Lys Ser	
	240 245 250	
	gac ttc gac aaa cat aca gat aga ttt cta agc tta gaa ggt gac aga	878
35	Asp Phe Asp Lys His Thr Asp Arg Phe Leu Ser Leu Glu Gly Asp Arg	

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	255	260	265	
	gcc aaa gtt ctg aag aca gtg act ttt gca aat gat cta aaa cca aag			926
	Ala Lys Val Leu Lys Thr Val Thr Phe Ala Asn Asp Leu Lys Pro Lys			
	270	275	280	
5	gtg tat aat cta aag aag gac ttt tcc cgt tta gaa cca tta gta aat			974
	Val Tyr Asn Leu Lys Lys Asp Phe Ser Arg Leu Glu Pro Leu Val Asn			
	285	290	295	
	gat tta aca cta cgc att ggg aga ttg gtt acc gac tta cta caa aga			1022
	Asp Leu Thr Leu Arg Ile Gly Arg Leu Val Thr Asp Leu Leu Gln Arg			
10	300	305	310	315
	gag aaa gaa att gct ttc tta agt gaa aaa ata tct aat tta aca ata			1070
	Glu Lys Glu Ile Ala Phe Leu Ser Glu Lys Ile Ser Asn Leu Thr Ile			
	320	325	330	
	gtc caa gct gag att aag gat att aaa gat gaa ata gca cac att tca			1118
15	Val Gln Ala Glu Ile Lys Asp Ile Lys Asp Glu Ile Ala His Ile Ser			
	335	340	345	
	gat atg aat tagtttgaca ttattgagat tagactaagg taattttttt aat			1170
	Asp Met Asn			
	350			
20	gggacctctc atgagaagac tggtaaatca aaaataatga tattttggag caaaagtcac			1230
	tttatattta atcctatattt gtacagtaaa aataaaaactt taaaacaggt tgattttcca			1290
	aaataaatat gctaaaacct			1310
	<210> 120			
25	<211> 1400			
	<212> DNA			
	<213> Homo Sapience			
	<220>			
	<221> CDS			
30	<222> (233)...(556)			
	<400> 120			
	tggtctgatg ctattggagg gtggaaatca catctoctgt ttatccgtgt gcttgtagg			60
	tgtcagccgc ccccccccc ccatatgcag atttactcgg catggtagtg gccagcttct			120
35	aacacagctg gtatttcaag tctcctggga cctcactcag gaatgatacc cctcagtag			180

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	aagcagcagg tgatcttaac tcctttcaaaa gagcaggcct gtctgggaag cc atg	235
	Met	
	1	
	tcc tca gca ggc aca gca acc cct ctg gaa atg gat cac aaa ctc act	283
5	Ser Ser Ala Gly Thr Ala Thr Pro Leu Glu Met Asp His Lys Leu Thr	
	5 10 15	
	tct cag cca ggc agg cca agc ttc tat tgt aac agt agg cac agt ata	331
	Ser Gln Pro Gly Arg Pro Ser Phe Tyr Cys Asn Ser Arg His Ser Ile	
	20 25 30	
10	gtc gga tca tca cat cag ctg ggt ttt tgg ttt agt cat cta gag tcg	379
	Val Gly Ser Ser His Gln Leu Gly Phe Trp Phe Ser His Leu Glu Ser	
	35 40 45	
	tct gga cta aag gtc ttt cag gtc tcc ttg ccc tgt gag tgc gtg aac	427
	Ser Gly Leu Lys Val Phe Gln Val Ser Leu Pro Cys Glu Cys Val Asn	
15	50 55 60 65	
	ctc ccc acc cga att gcc tca gtt gtc ctg agc ctc atg tot ctc ctg	475
	Leu Pro Thr Arg Ile Ala Ser Val Val Leu Ser Leu Met Ser Leu Leu	
	70 75 80	
	gtg gtg ggc cag gcc cct gca tgg gaa ggg agc ctg ctg cgg ggc agg	523
20	Val Val Gly Gln Ala Pro Ala Trp Glu Gly Ser Leu Leu Arg Gly Arg	
	85 90 95	
	cca gct ggg ggt gct cac cta tgc gca gca tgaagttatt gaaggac	570
	Pro Ala Gly Gly Ala His Leu Cys Ala Ala	
	100 105	
25	tggttggtga tggtggtgag cgtatccttc atggccagcg cgaagtcggc caggtcagcc	630
	aggtgctgcc agcgtctct ctcggacttg tcttcctgtg ccaggggacc gtggagaaag	690
	tgtcaggggc cgtcactgc agcagcctgc tctgtgcct tccttggcag tgttctgggg	750
	gtggattccc tacacctaga tggtcaaggc cttacttttc ctcccacaaa ggagtcgcag	810
	ccacgctagc tctgacttgc cactgtgaca aagttcacgt agcaggtcta ggcaaagact	870
30	gggcaattga gcagaggaga cggacctgtg agtctgacca cgaggcggac cccttcacct	930
	tggctgggcc tggctctggt ccttaggttt tgtcagggtg tccttggttg gatccctcaa	990
	ctaggtgata agcactggag ggggatgacc cgccttggaac gtgtttcttt aacctcatcc	1050
	atataatagg gccgtgggat gggtgtagag gtaaagcagg atgatggtgt ttttaagacca	1110
	gagcttgga ccagggctcc tacacctaat tttctctcct ggtagctgaa caaaggtcta	1170
35	aattagctta acaaaagaac aggctgccgt cagccagagt tctgaaggcc atgctttcag	1230

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tttcccttgt tgacaattgc tctccagttc ctatgaaagc acagagcctt aggggggcctg 1290
gccacagaac acaaccatct taggcctgag ctgtgaacag caggggggttg tgtgtctgtt 1350
ctgtttctct gcttgccgaa cttttctcaat aaaccctatt tcttatttat 1400

5 <210> 121
<211> 483
<212> PRT
<213> Homo sapience

10 <400> 121
Met Lys Ala Phe His Thr Phe Cys Val Val Leu Leu Val Phe Gly Ser
1 5 10 15
Val Ser Glu Ala Lys Phe Asp Asp Phe Glu Asp Glu Glu Asp Ile Val
20 25 30
15 Glu Tyr Asp Asp Asn Asp Phe Ala Glu Phe Glu Asp Val Met Glu Asp
35 40 45
Ser Val Thr Glu Ser Pro Gln Arg Val Ile Ile Thr Glu Asp Asp Glu
50 55 60
Asp Glu Thr Thr Val Glu Leu Glu Gly Gln Asp Glu Asn Gln Glu Gly
20 65 70 75 80
Asp Phe Glu Asp Ala Asp Thr Gln Glu Gly Asp Thr Glu Ser Glu Pro
85 90 95
Tyr Asp Asp Glu Glu Phe Glu Gly Tyr Glu Asp Lys Pro Asp Thr Ser
100 105 110
25 Ser Ser Lys Asn Lys Asp Pro Ile Thr Ile Val Asp Val Pro Ala His
115 120 125
Leu Gln Asn Ser Trp Glu Ser Tyr Tyr Leu Glu Ile Leu Met Val Thr
130 135 140
Gly Leu Leu Ala Tyr Ile Met Asn Tyr Ile Ile Gly Lys Asn Lys Asn
30 145 150 155 160
Ser Arg Leu Ala Gln Ala Trp Phe Asn Thr His Arg Glu Leu Leu Glu
165 170 175
Ser Asn Phe Thr Leu Val Gly Asp Asp Gly Thr Asn Lys Glu Ala Thr
180 185 190
35 Ser Thr Gly Lys Leu Asn Gln Glu Asn Glu His Ile Tyr Asn Leu Trp

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	195	200	205
	Cys Ser Gly Arg Val Cys Cys Glu Gly Met Leu Ile Gln Leu Arg Phe		
	210	215	220
5	Leu Lys Arg Gln Asp Leu Leu Asn Val Leu Ala Arg Met Met Arg Pro		
	225	230	235
	Val Ser Asp Gln Val Gln Ile Lys Val Thr Met Asn Asp Glu Asp Met		
	245	250	255
	Asp Thr Tyr Val Phe Ala Val Gly Thr Arg Lys Ala Leu Val Arg Leu		
	260	265	270
10	Gln Lys Glu Met Gln Asp Leu Ser Glu Phe Cys Ser Asp Lys Pro Lys		
	275	280	285
	Ser Gly Ala Lys Tyr Gly Leu Pro Asp Ser Leu Ala Ile Leu Ser Glu		
	290	295	300
	Met Gly Glu Val Thr Asp Gly Met Met Asp Thr Lys Met Val His Phe		
15	305	310	315
	Leu Thr His Tyr Ala Asp Lys Ile Glu Ser Val His Phe Ser Asp Gln		
	325	330	335
	Phe Ser Gly Pro Lys Ile Met Gln Glu Glu Gly Gln Pro Leu Lys Leu		
	340	345	350
20	Pro Asp Thr Lys Arg Thr Leu Leu Phe Thr Phe Asn Val Pro Gly Ser		
	355	360	365
	Gly Asn Thr Tyr Pro Lys Asp Met Glu Ala Leu Leu Pro Leu Met Asn		
	370	375	380
	Met Val Ile Tyr Ser Ile Asp Lys Ala Lys Lys Phe Arg Leu Asn Arg		
25	385	390	395
	Glu Gly Lys Gln Lys Ala Asp Lys Asn Arg Ala Arg Val Glu Glu Asn		
	405	410	415
	Phe Leu Lys Leu Thr His Val Gln Arg Gln Glu Ala Ala Gln Ser Arg		
	420	425	430
30	Arg Glu Glu Lys Lys Arg Ala Glu Lys Glu Arg Ile Met Asn Glu Glu		
	435	440	445
	Asp Pro Glu Lys Gln Arg Arg Leu Glu Glu Ala Ala Leu Arg Arg Glu		
	450	455	460
	Gln Lys Lys Leu Glu Lys Lys Gln Met Lys Met Lys Gln Ile Lys Val		
35	465	470	475
			480

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Lys Ala Met

<210> 122

<211> 334

5 <212> PRT

<213> Homo sapience

<400> 122

Met Val Glu Phe Ala Pro Leu Phe Met Pro Trp Glu Arg Arg Leu Gln
 10 1 5 10 15
 Thr Leu Ala Val Leu Gln Phe Val Phe Ser Phe Leu Ala Leu Ala Glu
 20 25 30
 Ile Cys Thr Val Gly Phe Ile Ala Leu Leu Phe Thr Arg Phe Trp Leu
 35 40 45
 15 Leu Thr Val Leu Tyr Ala Ala Trp Trp Tyr Leu Asp Arg Asp Lys Pro
 50 55 60
 Arg Gln Gly Gly Arg His Ile Gln Ala Ile Arg Cys Trp Thr Ile Trp
 65 70 75 80
 Lys Tyr Met Lys Asp Tyr Phe Pro Ile Ser Leu Val Lys Thr Ala Glu
 20 85 90 95
 Leu Asp Pro Ser Arg Asn Tyr Ile Ala Gly Phe His Pro His Gly Val
 100 105 110
 Leu Ala Val Gly Ala Phe Ala Asn Leu Cys Thr Glu Ser Thr Gly Phe
 115 120 125
 25 Ser Ser Ile Phe Pro Gly Ile Arg Pro His Leu Met Met Leu Thr Leu
 130 135 140
 Trp Phe Arg Ala Pro Phe Phe Arg Asp Tyr Ile Met Ser Ala Gly Leu
 145 150 155 160
 Val Thr Ser Glu Lys Glu Ser Ala Ala His Ile Leu Asn Arg Lys Gly
 30 165 170 175
 Gly Gly Asn Leu Leu Gly Ile Ile Val Gly Gly Ala Gln Glu Ala Leu
 180 185 190
 Asp Ala Arg Pro Gly Ser Phe Thr Leu Leu Leu Arg Asn Arg Lys Gly
 195 200 205
 35 Phe Val Arg Leu Ala Leu Thr His Gly Ala Pro Leu Val Pro Ile Phe

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210 215 220
 Ser Phe Gly Glu Asn Asp Leu Phe Asp Gln Ile Pro Asn Ser Ser Gly
 225 230 235 240
 Ser Trp Leu Arg Tyr Ile Gln Asn Arg Leu Gln Lys Ile Met Gly Ile
 5 245 250 255
 Ser Leu Pro Leu Phe His Gly Arg Gly Val Phe Gln Tyr Ser Phe Gly
 260 265 270
 Leu Ile Pro Tyr Arg Arg Pro Ile Thr Thr Val Val Gly Lys Pro Ile
 275 280 285
 10 Glu Val Gln Lys Thr Leu His Pro Ser Glu Glu Glu Val Asn Gln Leu
 290 295 300
 His Gln Arg Tyr Ile Lys Glu Leu Cys Asn Leu Phe Glu Ala His Lys
 305 310 315 320
 Leu Lys Phe Asn Ile Pro Ala Asp Gln His Leu Glu Phe Cys
 15 325 330

 <210> 123
 <211> 267
 <212> PRT
 20 <213> Homo sapience

 <400> 123
 Met Ala Pro Trp Ala Leu Leu Ser Pro Gly Val Leu Val Arg Thr Gly
 1 5 10 15
 25 His Thr Val Leu Thr Trp Gly Ile Thr Leu Val Leu Phe Leu His Asp
 20 25 30
 Thr Glu Leu Arg Gln Trp Glu Glu Gln Gly Glu Leu Leu Leu Pro Leu
 35 40 45
 Thr Phe Leu Leu Leu Val Leu Gly Ser Leu Leu Leu Tyr Leu Ala Val
 30 50 55 60
 Ser Leu Met Asp Pro Gly Tyr Val Asn Val Gln Pro Gln Pro Gln Glu
 65 70 75 80
 Glu Leu Lys Glu Glu Gln Thr Ala Met Val Pro Pro Ala Ile Pro Leu
 85 90 95
 35 Arg Arg Cys Arg Tyr Cys Leu Val Leu Gln Pro Leu Arg Ala Arg His

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100 105 110
 Cys Arg Glu Cys Arg Arg Cys Val Arg Arg Tyr Asp His His Cys Pro
 115 120 125
 Trp Met Glu Asn Cys Val Gly Glu Arg Asn His Pro Leu Phe Val Val
 5 130 135 140
 Tyr Leu Ala Leu Gln Leu Val Val Leu Leu Trp Gly Leu Tyr Leu Ala
 145 150 155 160
 Trp Ser Gly Leu Arg Phe Phe Gln Pro Trp Gly Leu Trp Leu Arg Ser
 165 170 175
 10 Ser Gly Leu Leu Phe Ala Thr Phe Leu Leu Leu Ser Leu Phe Ser Leu
 180 185 190
 Val Ala Ser Leu Leu Leu Val Ser His Leu Tyr Leu Val Ala Ser Asn
 195 200 205
 Thr Thr Thr Trp Glu Phe Ile Ser Ser His Arg Ile Ala Tyr Leu Arg
 15 210 215 220
 Gln Arg Pro Ser Asn Pro Phe Asp Arg Gly Leu Thr Arg Asn Leu Ala
 225 230 235 240
 His Phe Phe Cys Gly Trp Pro Ser Gly Ser Trp Glu Thr Leu Trp Ala
 245 250 255
 20 Glu Glu Glu Glu Glu Gly Ser Ser Pro Ala Val
 260 265

 <210> 124
 <211> 106
 25 <212> PRT
 <213> Homo sapience

 <400> 124
 Met Ser Thr Asn Asn Met Ser Asp Pro Arg Arg Pro Asn Lys Val Leu
 30 1 5 10 15
 Arg Tyr Lys Pro Pro Pro Ser Glu Cys Asn Pro Ala Leu Asp Asp Pro
 20 25 30
 Thr Pro Asp Tyr Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly
 35 35 40 45
 Leu Met Leu Lys Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser

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50 55 60
 Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met
 65 70 75 80
 Met Ser Ser Phe Met Leu Ser Ile Ser Ala Val Val Met Ser Tyr Leu
 5 85 90 95
 Gln Asn Pro Gln Pro Met Thr Pro Pro Trp
 100 105

 <210> 125
 10 <211> 224
 <212> PRT
 <213> Homo sapience

 <400> 125
 15 Met Thr Leu Phe His Phe Gly Asn Cys Phe Ala Leu Ala Tyr Phe Pro
 1 5 10 15
 Tyr Phe Ile Thr Tyr Lys Cys Ser Gly Leu Ser Glu Tyr Asn Ala Phe
 20 20 25 30
 Trp Lys Cys Val Gln Ala Gly Val Thr Tyr Leu Phe Val Gln Leu Cys
 20 35 40 45
 Lys Met Leu Phe Leu Ala Thr Phe Phe Pro Thr Trp Glu Gly Gly Ile
 50 55 60
 Tyr Asp Phe Ile Gly Glu Phe Met Lys Ala Ser Val Asp Val Ala Asp
 65 70 75 80
 25 Leu Ile Gly Leu Asn Leu Val Met Ser Arg Asn Ala Gly Lys Gly Glu
 85 90 95
 Tyr Lys Ile Met Val Ala Ala Leu Gly Trp Ala Thr Ala Glu Leu Ile
 100 105 110
 Met Ser Arg Cys Ile Pro Leu Trp Val Gly Ala Arg Gly Ile Glu Phe
 30 115 120 125
 Asp Trp Lys Tyr Ile Gln Met Ser Ile Asp Ser Asn Ile Ser Leu Val
 130 135 140
 His Tyr Ile Val Ala Ser Ala Gln Val Trp Met Ile Thr Arg Tyr Asp
 145 150 155 160
 35 Leu Tyr His Thr Phe Arg Pro Ala Val Leu Leu Leu Met Phe Leu Ser

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165 170 175
 Val Tyr Lys Ala Phe Val Met Glu Thr Phe Val His Leu Cys Ser Leu
 180 185 190
 Gly Ser Trp Ala Ala Leu Leu Ala Arg Ala Val Val Thr Gly Leu Leu
 5 195 200 205
 Ala Leu Ser Thr Leu Ala Leu Tyr Val Ala Val Val Asn Val His Ser
 210 215 220

 <210> 126
 10 <211> 258
 <212> PRT
 <213> Homo sapience

 <400> 126
 15 Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
 1 5 10 15
 Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
 20 20 25 30
 Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
 20 35 40 45
 Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
 50 55 60
 Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
 65 70 75 80
 25 Arg Arg Ser Met Phe Leu Met Thr Cys Lys Pro Pro Leu Tyr Met Gly
 85 90 95
 Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys Thr Ile Asp Glu Glu Leu
 100 105 110
 Glu Arg Asp Lys Arg Val Thr Trp Ile Val Glu Phe Phe Ala Asn Trp
 30 115 120 125
 Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile Tyr Ala Asp Leu Ser Leu
 130 135 140
 Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly Lys Val Asp Val Gly Arg
 145 150 155 160
 35 Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val Ser Thr Ser Pro Leu Thr

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165 170 175
 Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln Gly Gly Lys Glu Ala Met
 180 185 190
 Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg Ala Val Ser Trp Thr Phe
 5 195 200 205
 Ser Glu Glu Asn Val Ile Arg Glu Phe Asn Leu Asn Glu Leu Tyr Gln
 210 215 220
 Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp Asn Ile Pro Glu Glu Gln
 225 230 235 240
 10 Pro Val Ala Ser Thr Pro Thr Thr Val Ser Asp Gly Glu Asn Lys Lys
 245 250 255
 Asp Lys

 <210> 127
 15 <211> 110
 <212> PRT
 <213> Homo sapience

 <400> 127
 20 Met Ala Ala Val Val Ala Lys Arg Glu Gly Pro Pro Phe Ile Ser Glu
 1 5 10 15
 Ala Ala Val Arg Gly Asn Ala Ala Val Leu Asp Tyr Cys Arg Thr Ser
 20 25 30
 Val Ser Ala Leu Ser Gly Ala Thr Ala Gly Ile Leu Gly Leu Thr Gly
 25 35 40 45
 Leu Tyr Gly Phe Ile Phe Tyr Leu Leu Ala Ser Val Leu Leu Ser Leu
 50 55 60
 Leu Leu Ile Leu Lys Ala Gly Arg Arg Trp Asn Lys Tyr Phe Lys Ser
 65 70 75 80
 30 Arg Arg Pro Leu Phe Thr Gly Gly Leu Ile Gly Gly Leu Phe Thr Tyr
 85 90 95
 Val Leu Phe Trp Thr Phe Leu Tyr Gly Met Val His Val Tyr
 100 105 110

 35 <210> 128

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<211> 91

<212> PRT

<213> Homo sapience

5 <400> 128

Met Val Tyr Ile Ser Asn Gly Gln Val Leu Asp Ser Arg Ser Gln Ser

1 5 10 15

Pro Trp Arg Leu Ser Leu Ile Thr Asp Phe Phe Trp Gly Ile Ala Glu

20 25 30

10 Phe Val Val Leu Phe Phe Lys Thr Leu Leu Gln Gln Asp Val Lys Lys

35 40 45

Arg Arg Ser Tyr Gly Asn Ser Ser Asp Ser Arg Tyr Asp Asp Gly Arg

50 55 60

Gly Pro Pro Gly Asn Pro Pro Arg Arg Met Gly Arg Ile Asn His Leu

15 65 70 75 80

Arg Gly Pro Ser Pro Pro Pro Met Ala Gly Gly

85 90

<210> 129

20 <211> 344

<212> PRT

<213> Homo sapience

<400> 129

25 Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro Leu Ser

1 5 10 15

Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu Ala Leu

20 25 30

Leu Leu Pro His Cys Gln Lys Leu Phe Val Tyr Asp Leu His Ala Val

30 35 40 45

Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile Ile Cys

50 55 60

Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr Asn Phe

65 70 75 80

35 Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser Phe Leu

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	85	90	95
	Leu Gly Ser Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu Ile Glu		
	100	105	110
5	Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu Pro Ser		
	115	120	125
	Gly Phe Leu Ala Pro Val Phe Ala Leu Phe Val Pro Phe Tyr Cys Ser		
	130	135	140
	Ile Pro Arg Val Gln Val Ala Gln Ile Leu Gly Pro Leu Ser Ile Thr		
	145	150	155
10	Asn Lys Thr Leu Ile Tyr Ile Leu Gly Leu Gln Leu Phe Thr Ser Gly		
	165	170	175
	Ser Tyr Ile Trp Ile Val Ala Ile Ser Gly Leu Met Ser Gly Leu Cys		
	180	185	190
15	Tyr Asp Ser Lys Met Phe Gln Val His Gln Val Leu Cys Ile Pro Ser		
	195	200	205
	Trp Met Ala Lys Phe Phe Ser Trp Thr Leu Glu Pro Ile Phe Ser Ser		
	210	215	220
	Ser Glu Pro Thr Ser Glu Ala Arg Ile Gly Met Gly Ala Thr Leu Asp		
	225	230	235
20	Ile Gln Arg Gln Gln Arg Met Glu Leu Leu Asp Arg Gln Leu Met Phe		
	245	250	255
	Ser Gln Phe Ala Gln Gly Arg Arg Gln Arg Gln Gln Gln Gly Gly Met		
	260	265	270
25	Ile Asn Trp Asn Arg Leu Phe Pro Pro Leu Arg Gln Arg Gln Asn Val		
	275	280	285
	Asn Tyr Gln Gly Gly Arg Gln Ser Glu Pro Ala Ala Pro Pro Leu Glu		
	290	295	300
	Val Ser Glu Glu Gln Val Ala Arg Leu Met Glu Met Gly Phe Ser Arg		
	305	310	315
30	Gly Asp Ala Leu Glu Ala Leu Arg Ala Ser Asn Asn Asp Leu Asn Val		
	325	330	335
	Ala Thr Asn Phe Leu Leu Gln His		
	340		
35	<210> 130		

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<211> 428

<212> PRT

<213> Homo sapience

5

<400> 130

Met	Gly	Pro	Pro	Pro	Gly	Ala	Gly	Val	Ser	Cys	Arg	Gly	Gly	Cys	Gly	
1				5				10					15			
Phe	Ser	Arg	Leu	Leu	Ala	Trp	Cys	Phe	Leu	Leu	Ala	Leu	Ser	Pro	Gln	
			20				25						30			
10	Ala	Pro	Gly	Ser	Arg	Gly	Ala	Glu	Ala	Val	Trp	Thr	Ala	Tyr	Leu	Asn
			35				40						45			
Val	Ser	Trp	Arg	Val	Pro	His	Thr	Gly	Val	Asn	Arg	Thr	Val	Trp	Glu	
		50				55				60						
Leu	Ser	Glu	Glu	Gly	Val	Tyr	Gly	Gln	Asp	Ser	Pro	Leu	Glu	Pro	Val	
15	65				70				75				80			
Ala	Gly	Val	Leu	Val	Pro	Pro	Asp	Gly	Pro	Gly	Ala	Leu	Asn	Ala	Cys	
				85					90				95			
Asn	Pro	His	Thr	Asn	Phe	Thr	Val	Pro	Thr	Val	Trp	Gly	Ser	Thr	Val	
			100					105					110			
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			115					120					125			
Ala	Asp	Lys	Ile	His	Leu	Ala	Tyr	Glu	Arg	Gly	Ala	Ser	Gly	Ala	Val	
		130				135					140					
Ile	Phe	Asn	Phe	Pro	Gly	Thr	Arg	Asn	Glu	Val	Ile	Pro	Met	Ser	His	
25	145				150				155				160			
Pro	Gly	Ala	Val	Asp	Ile	Val	Ala	Ile	Met	Ile	Gly	Asn	Leu	Lys	Gly	
			165					170					175			
Thr	Lys	Ile	Leu	Gln	Ser	Ile	Gln	Arg	Gly	Ile	Gln	Val	Thr	Met	Val	
			180					185					190			
30	Ile	Glu	Val	Gly	Lys	Lys	His	Gly	Pro	Trp	Val	Asn	His	Tyr	Ser	Ile
			195					200					205			
Phe	Phe	Val	Ser	Val	Ser	Phe	Phe	Ile	Ile	Thr	Ala	Ala	Thr	Val	Gly	
		210				215					220					
Tyr	Phe	Ile	Phe	Tyr	Ser	Ala	Arg	Arg	Leu	Arg	Asn	Ala	Arg	Ala	Gln	
35	225					230				235				240		

	Ser Arg Lys Gln Arg Gln Leu Lys Ala Asp Ala Lys Lys Ala Ile Gly			
	245	250	255	
	Arg Leu Gln Leu Arg Thr Leu Lys Gln Gly Asp Lys Glu Ile Gly Pro			
	260	265	270	
5	Asp Gly Asp Ser Cys Ala Val Cys Ile Glu Leu Tyr Lys Pro Asn Asp			
	275	280	285	
	Leu Val Arg Ile Leu Thr Cys Asn His Ile Phe His Lys Thr Cys Val			
	290	295	300	
	Asp Pro Trp Leu Leu Glu His Arg Thr Cys Pro Met Cys Lys Cys Asp			
10	305	310	315	320
	Ile Leu Lys Ala Leu Gly Ile Glu Val Asp Val Glu Asp Gly Ser Val			
	325	330	335	
	Ser Leu Gln Val Pro Val Ser Asn Glu Ile Ser Asn Ser Ala Ser Ser			
	340	345	350	
15	His Glu Glu Asp Asn Arg Ser Glu Thr Ala Ser Ser Gly Tyr Ala Ser			
	355	360	365	
	Val Gln Gly Thr Asp Glu Pro Pro Leu Glu Glu His Val Gln Ser Thr			
	370	375	380	
	Asn Glu Ser Leu Gln Leu Val Asn His Glu Ala Asn Ser Val Ala Val			
20	385	390	395	400
	Asp Val Ile Pro His Val Asp Asn Pro Thr Phe Glu Glu Asp Glu Thr			
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	gaatttgagg atgtcatgga agactctggt actgaatctc ctcaacgggt cataatcact		180	
35	qaaqatgatq aaqatqaqac cactgtggaq ttggaagggc aggatgaaaa ccaagaagga		240	

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	g a a t t t g a a g g t t a t g a a g a c a a c c a g a t a c t t c t t c t a g c a a a a t a a a g a c c c a a t a	360
	a c g a t t g t t g a t g t t c c t g c a c a c c t c c a g a a c a g c t g g g a g a g t t a t t a t c t a g a a a t t	420
	t t g a t g g t g a c t g g t c t g c t t g e t t a t a t c a t g a a t t a c a t c a t t g g g a a g a a t a a a a c	480
5	a g t c g c c t t g c a c a g g c c t g g t t t a a c a c t c a t a g g g a g c t t t t g g a g a g c a a c t t t a c t	540
	t t a g t g g g g g a t g a t g g a a c t a a c a a g a a g c c a c a a g c a c a g g a a g t t g a a c c a g g a g	600
	a a t g a g c a c a t c t a t a a c c t g t g g t g t t c t g g t c g a g t g t g c t g t g a g g g c a t g c t t a t c	660
	c a g c t g a g g t t c c t c a a g a g a c a a g a c t t a c t g a a t g t c c t g g c c g g a t g a t g a g g c c a	720
	g t g a g t g a t c a a g t g c a a a t a a a a g t a a c c a t g a a t g a t g a a g a c a t g g a t a c c t a c g t a	780
10	t t t g c t g t t g g c a c a c g g a a a g c c t t g g t g c g a c t a c a g a a a g a g a t g c a g g a t t t g a g t	840
	g a g t t t t g t a g t g a t a a c c t a a g t c t g g a g c a a a g t a t g g a c t g c c g g a c t c t t t g g c c	900
	a t c c t g t c a g a g a t g g g a g a g t c a c a g a c g g a a t g a t g g a t a c a a a g a t g g t t c a c t t t	960
	c t t a c a c a c t a t g c t g a c a a g a t t g a a t c t g t t c a t t t t c a g a c c a g t t c t c t g g t c c a	1020
	a a a a t t a t g c a a g a g g a a g g t c a g c c t t t a a a g t a c c t g a c a c t a a g a g g a c a c t g t t g	1080
15	t t t a c a t t t a a t g t g c c t g g c t c a g g t a a c a c t t a c c c a a a g g a t a t g g a g g c a c t g c t a	1140
	c c c c t g a t g a a c a t g g t g a t t t a t t c t a t t g a t a a a g c c a a a a g t t c c g a c t c a a c a g a	1200
	g a a g g c a a a c a a a a a g c a g a t a a g a a c c g t g c c c g a g t a g a a g a g a a c t t c t t g a a a c t g	1260
	a c a c a t g t g c a a a g a c a g g a a g c a g c a c a g t c t c g g c g g g a g g a g a a a a a a a g a g c a g a g	1320
	a a g g a g c g a a t c a t g a a t g a g g a a g a t c c t g a g a a c a g c g c a g g c t g g a g g a g g c t g c a	1380
20	t t g a g g c g t g a g c a a a a g a a g t t g g a a a a g a a g c a a a t g a a a t g a a a c a a a t c a a a g t g	1440
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30	c t a c a g t t t g t c t t c t c c t t c t t g g c a c t g g c g a g a t c t g c a c t g t g g g c t t c a t a g c c	120
	c t c c t g t t t a c a a g a t t c t g g t c c t c a c t g t c c t g t a t g c g g c c t g g t g g t a t c t g g a c	180
	c g a g a c a a g c c a c g g c a g g g g g c c g g c a c a t c c a g g c c a t c a g g t g c t g a c t a t a t g g	240
	a a g t a c a t g a a g g a c t a t t t c c c c a t c t c g c t g g t c a a g a c t g c t g a g c t g g a c c c c t c t	300
	c g g a a c t a c a t t g c g g g c t t c c a c c c c c a t g g a g t c c t g g c a g t c g g a g c c t t t g c c a a c	360
35	c t g t g c a c t g a g a g c a c a g g c t t c t c t t c t g a t c t t c c c c g g t a t c c g c c c c a t c t g a t g	420

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<210> 134

<211> 318

35 <212> DNA

153/177

<213> Homo sapience

<400> 134

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 ggcatgatct tcagcatgtg cggcctcatg cttaagctga agtgggtgtgc ttgggtgctg 180
 gtctactgct ccttcacacg ctttgccaac tctcggagct cggaggacac gaagcaaagt 240
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15

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 acctacctct ttgtccaact ctgcaagatg ctgttcttgg ccactttctt tcccacctgg 180
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30

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<211> 774

<212> DNA

<213> Homo sapience

35

<400> 136

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	gagctatacc agcggggcaa gaaactatca aaggctggag acaatatccc tgaggagcag	720
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35 <400> 140

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	tctggagcgg tcatctttaa cttccccggg acccgcaatg aggtcaccac catgtctcac	480
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Met Lys Ala Phe His Thr Phe Cys Val Val Leu Leu Val Phe Gly

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	Val Glu Tyr Asp Asp Asn Asp Phe Ala Glu Phe Glu Asp Val Met Glu				
	35	40	45		
	gac tct gtt act gaa tct cct caa cgg gtc ata atc act gaa gat gat	310			
10	Asp Ser Val Thr Glu Ser Pro Gln Arg Val Ile Ile Thr Glu Asp Asp				
	50	55	60		
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	Glu Asp Glu Thr Thr Val Glu Leu Glu Gly Gln Asp Glu Asn Gln Glu				
	65	70	75		
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	Gly Asp Phe Glu Asp Ala Asp Thr Gln Glu Gly Asp Thr Glu Ser Glu				
	80	85	90	95	
	cca tat gat gat gaa gaa ttt gaa ggt tat gaa gac aaa cca gat act	454			
	Pro Tyr Asp Asp Glu Glu Phe Glu Gly Tyr Glu Asp Lys Pro Asp Thr				
20		100	105	110	
	tct tct agc aaa aat aaa gac cca ata acg att gtt gat gtt cct gca	502			
	Ser Ser Ser Lys Asn Lys Asp Pro Ile Thr Ile Val Asp Val Pro Ala				
	115	120	125		
	cac etc cag aac agc tgg gag agt tat tat cta gaa att ttg atg gtg	550			
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	130	135	140		
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	Thr Gly Leu Leu Ala Tyr Ile Met Asn Tyr Ile Ile Gly Lys Asn Lys				
	145	150	155		
30	aac agt cgc ctt gca cag gcc tgg ttt aac act cat agg gag ctt ttg	646			
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35		180	185	190	

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	ttc ctc aag aga caa gac tta ctg aat gtc ctg gcc cgg atg atg agg	838
	Phe Leu Lys Arg Gln Asp Leu Leu Asn Val Leu Ala Arg Met Met Arg	
	225 230 235	
10	cca gtg agt gat caa gtg caa ata aaa gta acc atg aat gat gaa gac	886
	Pro Val Ser Asp Gln Val Gln Ile Lys Val Thr Met Asn Asp Glu Asp	
	240 245 250 255	
	atg gat acc tac gta ttt gct gtt ggc aca cgg aaa gcc ttg gtg cga	934
	Met Asp Thr Tyr Val Phe Ala Val Gly Thr Arg Lys Ala Leu Val Arg	
15	260 265 270	
	cta cag aaa gag atg cag gat ttg agt gag ttt tgt agt gat aaa cct	982
	Leu Gln Lys Glu Met Gln Asp Leu Ser Glu Phe Cys Ser Asp Lys Pro	
	275 280 285	
	aag tct gga gca aag tat gga ctg ccg gac tct ttg gcc atc ctg tca	1030
20	Lys Ser Gly Ala Lys Tyr Gly Leu Pro Asp Ser Leu Ala Ile Leu Ser	
	290 295 300	
	gag atg gga gaa gtc aca gac gga atg atg gat aca aag atg gtt cac	1078
	Glu Met Gly Glu Val Thr Asp Gly Met Met Asp Thr Lys Met Val His	
	305 310 315	
25	ttt ctt aca cac tat gct gac aag att gaa tct gtt cat ttt tca gac	1126
	Phe Leu Thr His Tyr Ala Asp Lys Ile Glu Ser Val His Phe Ser Asp	
	320 325 330 335	
	cag ttc tct ggt cca aaa att atg caa gag gaa ggt cag cct tta aag	1174
	Gln Phe Ser Gly Pro Lys Ile Met Gln Glu Glu Gly Gln Pro Leu Lys	
30	340 345 350	
	cta cct gac act aag agg aca ctg ttg ttt aca ttt aat gtg cct ggc	1222
	Leu Pro Asp Thr Lys Arg Thr Leu Leu Phe Thr Phe Asn Val Pro Gly	
	355 360 365	
	tca ggt aac act tac cca aag gat atg gag gca ctg cta ccc ctg atg	1270
35	Ser Gly Asn Thr Tyr Pro Lys Asp Met Glu Ala Leu Leu Pro Leu Met	

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	370	375	380	
	aac atg gtg att tat tct att gat aaa gcc aaa aag ttc cga ctc aac			1318
	Asn Met Val Ile Tyr Ser Ile Asp Lys Ala Lys Lys Phe Arg Leu Asn			
	385	390	395	
5	aga gaa ggc aaa caa aaa gca gat aag aac cgt gcc cga gta gaa gag			1366
	Arg Glu Gly Lys Gln Lys Ala Asp Lys Asn Arg Ala Arg Val Glu Glu			
	400	405	410	415
	aac ttc ttg aaa ctg aca cat gtg caa aga cag gaa gca gca cag tct			1414
	Asn Phe Leu Lys Leu Thr His Val Gln Arg Gln Glu Ala Ala Gln Ser			
10	420	425	430	
	cgg cgg gag gag aaa aaa aga gca gag aag gag cga atc atg aat gag			1462
	Arg Arg Glu Glu Lys Lys Arg Ala Glu Lys Glu Arg Ile Met Asn Glu			
	435	440	445	
	gaa gat cct gag aaa cag cgc agg ctg gag gag gct gca ttg agg cgt			1510
15	Glu Asp Pro Glu Lys Gln Arg Arg Leu Glu Glu Ala Ala Leu Arg Arg			
	450	455	460	
	gag caa aag aag ttg gaa aag aag caa atg aaa atg aaa caa atc aaa			1558
	Glu Gln Lys Lys Leu Glu Lys Lys Gln Met Lys Met Lys Gln Ile Lys			
	465	470	475	
20	gtg aaa gcc atg taaagccatc ccagagattt gagttctgat gccacctgta			1610
	Val Lys Ala Met			
	480			
	agctctgaat tcacaggaaa catgaaaaac gccagtccat ttctcaacct taaatttcag			1670
	acagtcttgg gcaactgaga aatccttatt tcatacatcta ctctgtttgg gggttgggggt			1730
25	tttacagaga ttgaagatac ctggaaaggg ctctgtttca agaatttttt tttccagata			1790
	atcaaattat ttgtattatt ttataaaagg aatgatctat gaaatctgtg taggttttaa			1850
	atattttaaa aattataata caaatcatca gtgttttttag tacttcagtg tttaaagaaa			1910
	taccatgaaa tttataggta gataaccaga ttgttgcttt ttgttttaaac caagcagttg			1970
	aaatggctat aaagactgac tctaaaccaa gattctgcaa ataatgattg gaattgcaca			2030
30	ataaacattg cttgatgttt			2050
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	<211> 2746			
	<212> DNA			
35	<213> Homo sapience			

160/177

<220>

<221> CDS

<222> (70)...(1074)

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cccgccagc atg gta gag ttc gcg ccc ttg ttt atg ccg tgg gag cgc 108

Met Val Glu Phe Ala Pro Leu Phe Met Pro Trp Glu Arg

1

5

10

10 agg ctg cag aca ctt gct gtc cta cag ttt gtc ttc tcc ttc ttg gca 156

Arg Leu Gln Thr Leu Ala Val Leu Gln Phe Val Phe Ser Phe Leu Ala

15

20

25

ctg gcc gag atc tgc act gtg ggc ttc ata gcc ctc ctg ttt aca aga 204

Leu Ala Glu Ile Cys Thr Val Gly Phe Ile Ala Leu Leu Phe Thr Arg

15 30 35 40 45

ttc tgg ctc ctc act gtc ctg tat gcg gcc tgg tgg tat ctg gac cga 252

Phe Trp Leu Leu Thr Val Leu Tyr Ala Ala Trp Trp Tyr Leu Asp Arg

50

55

60

gac aag cca cgg cag ggg ggc cgg cac atc cag gcc atc agg tgc tgg 300

20 Asp Lys Pro Arg Gln Gly Gly Arg His Ile Gln Ala Ile Arg Cys Trp

65

70

75

act ata tgg aag tac atg aag gac tat ttc ccc atc tcg ctg gtc aag 348

Thr Ile Trp Lys Tyr Met Lys Asp Tyr Phe Pro Ile Ser Leu Val Lys

80

85

90

25 act gct gag ctg gac ccc tct cgg aac tac att gcg ggc ttc cac ccc 396

Thr Ala Glu Leu Asp Pro Ser Arg Asn Tyr Ile Ala Gly Phe His Pro

95

100

105

cat gga gtc ctg gca gtc gga gcc ttt gcc aac ctg tgc act gag agc 444

His Gly Val Leu Ala Val Gly Ala Phe Ala Asn Leu Cys Thr Glu Ser

30 110 115 120 125

aca ggc ttc tct tcg atc ttc ccc ggt atc cgc ccc cat ctg atg atg 492

Thr Gly Phe Ser Ser Ile Phe Pro Gly Ile Arg Pro His Leu Met Met

130

135

140

ctg acc ttg tgg ttc cgg gcc ccc ttc ttc aga gat tac atc atg tct 540

35 Leu Thr Leu Trp Phe Arg Ala Pro Phe Phe Arg Asp Tyr Ile Met Ser

161/177

	145	150	155	
	gca ggg ttg gtc aca tca gaa aag gag agt gct gct cac att ctg aac			588
	Ala Gly Leu Val Thr Ser Glu Lys Glu Ser Ala Ala His Ile Leu Asn			
	160	165	170	
5	agg aag ggt ggc gga aac ttg ctg ggc atc att gta ggg ggt gcc cag			636
	Arg Lys Gly Gly Gly Asn Leu Leu Gly Ile Ile Val Gly Gly Ala Gln			
	175	180	185	
	gag gcc ctg gat gcc agg cct gga tcc ttc acg ctg tta ctg cgg aac			684
	Glu Ala Leu Asp Ala Arg Pro Gly Ser Phe Thr Leu Leu Leu Arg Asn			
10	190	195	200	205
	cga aag ggc ttc gtc agg ctc gcc ctg aca cac ggg gca ccc ctg gtg			732
	Arg Lys Gly Phe Val Arg Leu Ala Leu Thr His Gly Ala Pro Leu Val			
	210	215	220	
	cca atc ttc tcc ttc ggg gag aat gac cta ttt gac cag att ccc aac			780
15	Pro Ile Phe Ser Phe Gly Glu Asn Asp Leu Phe Asp Gln Ile Pro Asn			
	225	230	235	
	tct tct ggc tcc tgg tta cgc tat atc cag aat cgg ttg cag aag atc			828
	Ser Ser Gly Ser Trp Leu Arg Tyr Ile Gln Asn Arg Leu Gln Lys Ile			
	240	245	250	
20	atg ggc atc tcc ctc cca ctc ttt cat ggc cgt ggt gtc ttc cag tac			876
	Met Gly Ile Ser Leu Pro Leu Phe His Gly Arg Gly Val Phe Gln Tyr			
	255	260	265	
	agc ttt ggt tta ata ccc tac cgc cgg ccc atc acc act gtg gtg ggg			924
	Ser Phe Gly Leu Ile Pro Tyr Arg Arg Pro Ile Thr Thr Val Val Gly			
25	270	275	280	285
	aag ccc atc gag gta cag aag acg ctg cat ccc tcg gag gag gag gtg			972
	Lys Pro Ile Glu Val Gln Lys Thr Leu His Pro Ser Glu Glu Glu Val			
	290	295	300	
	aac cag ctg cac cag cgt tat atc aaa gag ctg tgc aac ctc ttc gag			1020
30	Asn Gln Leu His Gln Arg Tyr Ile Lys Glu Leu Cys Asn Leu Phe Glu			
	305	310	315	
	gcc cac aaa ctt aag ttc aac atc cct gct gac cag cac ttg gag ttc			1068
	Ala His Lys Leu Lys Phe Asn Ile Pro Ala Asp Gln His Leu Glu Phe			
	320	325	330	
35	tgc tgagcccaa agggcagggc caacattagg gagccagca ggaggtgctg			1120

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Cys

	tgctgagaag	acttcctgga	ggtgtttgtt	gaacatatct	gcagagcctt	cccagactcc	1180
	tgcaaatcca	acccatatca	ggtgttaagt	cagagcaggc	aatgcagaag	aggagaccag	1240
	accaaggggt	cagctggggc	taggacagt	agggctgcta	gaggggctgg	gcctctcttt	1300
5	gcacatggac	actgggcccc	tctctatatt	gagtggctctg	ttaacattca	ttggtggctg	1360
	attccaaaag	atgagageca	aagctgcacg	gactcgagtc	ctaggctgca	cacctcacia	1420
	gcactctctc	tactgcattc	tggtggctga	agcaagtcac	aaccagcag	attcaaggag	1480
	taaggaatag	gatccccctc	tggatgggag	gagcagcaat	gtcatattac	aaaaggggtg	1540
	ggacacatgc	agggattctt	actgccgtct	ttgcaaacia	tccacaaaaa	cttaaaaaact	1600
10	aaaagcctga	agcacaagca	ctctccaccc	caggcacaca	caccctggaa	ttccctgtgt	1660
	gaccatggta	ccaccactgt	gtgtcccgag	gatcccagct	cagctttgca	tcgctgccct	1720
	atctccctct	cgtctctccc	tggtgatccc	tcattgcacag	ccacagcgag	ctgtctaaaa	1780
	cacaaagctg	accgcgccat	ttctactca	gcactctcc	atgacctcc	attgctccta	1840
	ggataggggt	tggaccagtc	tgaatccaga	ggatcaggat	ccagcaggaa	ccagaggata	1900
15	atgtgaggag	ggtttaaaaa	ggaaccattt	tttgagggtg	gtgcactgtt	tccacctga	1960
	ggcctggaag	gatgaatgga	agcagcagtt	cctgaaccag	gaagactcat	gtgtgggggc	2020
	cattgctggt	caaggggcac	gaacaggtct	ggtgacctg	caagggagga	gccaggagca	2080
	agcattccca	cttcaccttc	ctccattcag	tctgctgcca	agttccccac	tgctgagcc	2140
	caactagaag	ctggagggaa	ggagggcctg	tggtctcagt	ccaggcatgt	aggcctcctg	2200
20	ggaaagggag	aatggcaaag	acaggcagag	tggatctgga	gggtcaacg	gaagacggaa	2260
	catgtccact	tccaggeccg	agcttctcag	cctgccgttt	gccactctcc	agcatctggc	2320
	ccagcctgtc	catctctatc	tctcttcttc	ccttactccg	tgctccccatc	actcggaacc	2380
	atgtgcattt	ctttgtctca	gctatattgt	ctcacctctg	agtttttgcc	catgatgttg	2440
	gatgccatgg	aatgccatat	cctccccatt	atctccccct	tgtctggata	attcctactc	2500
25	atcctacaat	actgatttta	tctgtgcaaa	gaagtcttcc	ccagtgcctc	tggttgacag	2560
	gggtttcttc	tggtttctcc	agactttctg	ttcctccacc	acagccctta	gcacctggg	2620
	gaggaggtgt	tgtgtctccag	gtaaatgtg	cgccaatgcc	cctgcctcta	gtgcactccc	2680
	tccagcctac	ccacaaacag	gacctgcac	ctgtctcaca	aataaaaactg	aactcttgaa	2740
	atggtg						2746

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<210> 143

<211> 1136

<212> DNA

<213> Homo sapiens

35

<220>

163/177

<221> CDS

<222> (32)...(835)

<400> 143

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	Met Ala Pro Trp Ala Leu Leu	
	1 5	
	agc cct ggg gtc ctg gtg cgg acc ggg cac acc gtg ctg acc tgg gga	100
	Ser Pro Gly Val Leu Val Arg Thr Gly His Thr Val Leu Thr Trp Gly	
10	10 15 20	
	atc acg ctg gtg ctc ttc ctg cac gat acc gag ctg cgg caa tgg gag	148
	Ile Thr Leu Val Leu Phe Leu His Asp Thr Glu Leu Arg Gln Trp Glu	
	25 30 35	
	gag cag ggg gag ctg ctc ctg ccc ctc acc ttc ctg ctc ctg gtg ctg	196
15	Glu Gln Gly Glu Leu Leu Leu Pro Leu Thr Phe Leu Leu Leu Val Leu	
	40 45 50 55	
	ggc tcc ctg ctg ctc tac ctc gct gtg tca ctc atg gac cct ggc tac	244
	Gly Ser Leu Leu Leu Tyr Leu Ala Val Ser Leu Met Asp Pro Gly Tyr	
	60 65 70	
20	gtg aat gtg cag ccc cag cct cag gag gag ctc aaa gag gag cag aca	292
	Val Asn Val Gln Pro Gln Pro Gln Glu Leu Lys Glu Glu Gln Thr	
	75 80 85	
	gcc atg gtt cct cca gcc atc cct ctt cgg cgc tgc aga tac tgc ctg	340
	Ala Met Val Pro Pro Ala Ile Pro Leu Arg Arg Cys Arg Tyr Cys Leu	
25	90 95 100	
	gtg ctg cag ccc ctg agg gct cgg cac tgc cgt gag tgc cgc cgt tgc	388
	Val Leu Gln Pro Leu Arg Ala Arg His Cys Arg Glu Cys Arg Arg Cys	
	105 110 115	
	gtc cgc cgc tac gac cac cac tgc ccc tgg atg gag aac tgt gtg gga	436
30	Val Arg Arg Tyr Asp His His Cys Pro Trp Met Glu Asn Cys Val Gly	
	120 125 130 135	
	gag cgc aac cac cca ctc ttt gtg gtc tac ctg gcg ctg cag ctg gtg	484
	Glu Arg Asn His Pro Leu Phe Val Val Tyr Leu Ala Leu Gln Leu Val	
	140 145 150	
35	gtg ctt ctg tgg ggc ctg tac ctg gca tgg tca ggc ctc cgg ttc ttc	532

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	Val Leu Leu Trp Gly Leu Tyr Leu Ala Trp Ser Gly Leu Arg Phe Phe	
	155 160 165	
	cag ccc tgg ggt ctg tgg ttg cgg tcc agc ggg ctc ctg ttc gcc acc	580
	Gln Pro Trp Gly Leu Trp Leu Arg Ser Ser Gly Leu Leu Phe Ala Thr	
5	170 175 180	
	ttc ctg ctg ctg tcc ctc ttc tgg ttg gtg gcc agc ctg ctc ctc gtc	628
	Phe Leu Leu Leu Ser Leu Phe Ser Leu Val Ala Ser Leu Leu Leu Val	
	185 190 195	
	tgc cac ctc tac ctg gtg gcc agc aac acc acc acc tgg gaa ttc atc	676
10	Ser His Leu Tyr Leu Val Ala Ser Asn Thr Thr Thr Trp Glu Phe Ile	
	200 205 210 215	
	tcc tca cac cgc atc gcc tat ctc cgc cag cgc ccc agc aac ccc ttc	724
	Ser Ser His Arg Ile Ala Tyr Leu Arg Gln Arg Pro Ser Asn Pro Phe	
	220 225 230	
15	gac cga ggc ctg acc cgc aac ctg gcc cac ttc ttc tgt gga tgg ccc	772
	Asp Arg Gly Leu Thr Arg Asn Leu Ala His Phe Phe Cys Gly Trp Pro	
	235 240 245	
	tca ggg tcc tgg gag acc ctc tgg gct gag gag gag gaa gag gcc agc	820
	Ser Gly Ser Trp Glu Thr Leu Trp Ala Glu Glu Glu Glu Glu Gly Ser	
20	250 255 260	
	agc cca gct gtt taggggttgcct ggaggccggg ctaccgtctt gtgcctga	870
	Ser Pro Ala Val	
	265	
	aaaccacggg gcctgtcccc agctgggggtg agcgcctcaga gggcctgggg ccctcaactcc	930
25	tgccccacgcc tcccagaccc cagaacggag cttcaagtca gacagatccc tgccttggtg	990
	ggcagttctg ccttccaagg aagaagggga agaaaaggac ctgtgggtgg ctcaggccca	1050
	agcagacccc gggtccacc ccagcccgcc ccaggctgct gccagtgcac actttttacaa	1110
	atttaatatata aagcaagtcc agtctt	1136
30	<210> 144	
	<211> 619	
	<212> DNA	
	<213> Homo sapience	
	<220>	
35	<221> CDS	

165/177

<222> (13)...(333)

<400> 144

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 Met Ser Thr Asn Asn Met Ser Asp Pro Arg Arg Pro
 1 5 10
 aac aaa gtg ctg agg tac aag ccc ccg ccg agc gaa tgt aac ccg gcc 96
 Asn Lys Val Leu Arg Tyr Lys Pro Pro Pro Ser Glu Cys Asn Pro Ala
 15 20 25
 10 ttg gac gac ccg acg ccg gac tac atg aac ctg ctg ggc atg atc ttc 144
 Leu Asp Asp Pro Thr Pro Asp Tyr Met Asn Leu Leu Gly Met Ile Phe
 30 35 40
 agc atg tgc ggc ctc atg ctt aag ctg aag tgg tgt gct tgg gtc gct 192
 Ser Met Cys Gly Leu Met Leu Lys Leu Lys Trp Cys Ala Trp Val Ala
 15 45 50 55 60
 gtc tac tgc tcc ttc atc agc ttt gcc aac tct cgg agc tcg gag gac 240
 Val Tyr Cys Ser Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser Glu Asp
 65 70 75
 acg aag caa atg atg agt agc ttc atg ctg tcc atc tct gcc gtg gtg 288
 20 Thr Lys Gln Met Met Ser Ser Phe Met Leu Ser Ile Ser Ala Val Val
 80 85 90
 atg tcc tat ctg cag aat cct cag ccc atg acg ccc cca tgg 340
 Met Ser Tyr Leu Gln Asn Pro Gln Pro Met Thr Pro Pro Trp
 95 100 105
 25 tgataccagc ctagaagggt cacatttttg accctgtcta tccactaggc ctgggctttg 390
 gctgctaaac ctgctgcctt cagctgccat cctggacttc cctgaatgag gccgtctcgg 450
 tgccccccagc tggatagagg gaacctggcc ctttctagg gaacacccta ggcttaccoc 510
 tcctgcctcc ctccccctgc ctgctgctgg gggagatgct gtccatgttt ctaggggtat 570
 tcatttgctt tctcgttgaa acctgttggt aataaagttt ttcactcag 619
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<210> 145

<211> 864

<212> DNA

<213> Homo sapience

35 <220>

166/177

<221> CDS

<222> (111)...(785)

<400> 145

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	gagacgccgc ctccgatcc ccgcgcgggc gggaccgggc ggccggcacc atg acc	116
	Met Thr	
	1	
10	ctg ttt cac ttc ggg aac tgc ttc gct ctt gcc tac ttc ccc tac ttc	164
	Leu Phe His Phe Gly Asn Cys Phe Ala Leu Ala Tyr Phe Pro Tyr Phe	
	5 10 15	
	atc acc tac aag tgc agc ggc ctg tcc gag tac aac gcc ttc tgg aaa	212
	Ile Thr Tyr Lys Cys Ser Gly Leu Ser Glu Tyr Asn Ala Phe Trp Lys	
	20 25 30	
15	tgc gtc cag gct gga gtc acc tac ctc ttt gtc caa ctc tgc aag atg	260
	Cys Val Gln Ala Gly Val Thr Tyr Leu Phe Val Gln Leu Cys Lys Met	
	35 40 45 50	
	ctg ttc ttg gcc act ttc ttt ccc acc tgg gaa ggc ggc atc tat gac	308
	Leu Phe Leu Ala Thr Phe Phe Pro Thr Trp Glu Gly Gly Ile Tyr Asp	
20	55 60 65	
	ttc att ggg gag ttc atg aag gcc agc gtg gat gtg gca gac ctg ata	356
	Phe Ile Gly Glu Phe Met Lys Ala Ser Val Asp Val Ala Asp Leu Ile	
	70 75 80	
	ggc cta aac ctt gtc atg tcc cgg aat gcc ggc aag gga gag tac aag	404
25	Gly Leu Asn Leu Val Met Ser Arg Asn Ala Gly Lys Gly Glu Tyr Lys	
	85 90 95	
	atc atg gtt gct gcc ctg ggc tgg gcc act gct gag ctt att atg tcc	452
	Ile Met Val Ala Ala Leu Gly Trp Ala Thr Ala Glu Leu Ile Met Ser	
	100 105 110	
30	cgc tgc att ccc cta tgg gtc gga gcc cgg ggc att gag ttt gac tgg	500
	Arg Cys Ile Pro Leu Trp Val Gly Ala Arg Gly Ile Glu Phe Asp Trp	
	115 120 125 130	
	aag tac atc cag atg agc ata gac tcc aac atc agt ctg gtc cat tac	548
	Lys Tyr Ile Gln Met Ser Ile Asp Ser Asn Ile Ser Leu Val His Tyr	
35	135 140 145	

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atc gtc gcg tct gct cag gtc tgg atg ata aca cgc tat gat ctg tac 596
 Ile Val Ala Ser Ala Gln Val Trp Met Ile Thr Arg Tyr Asp Leu Tyr
 150 155 160
 cac acc ttc cgg cca gct gtc ctc ctg ctg atg ttc ctc agt gtc tac 644
 5 His Thr Phe Arg Pro Ala Val Leu Leu Met Phe Leu Ser Val Tyr
 165 170 175
 aag gcc ttt gtt atg gag acc ttc gtc cac ctc tgc tcg ctg ggc agt 692
 Lys Ala Phe Val Met Glu Thr Phe Val His Leu Cys Ser Leu Gly Ser
 180 185 190
 10 tgg gca gct cta ctg gcc cga gca gtg gta acg ggg ctg ctg gcc ctc 740
 Trp Ala Ala Leu Leu Ala Arg Ala Val Val Thr Gly Leu Leu Ala Leu
 195 200 205 210
 agc act ttg gcc ctg tat gtc gcc gtt gtc aat gtg cac tcc taggett 790
 Ser Thr Leu Ala Leu Tyr Val Ala Val Val Asn Val His Ser
 15 215 220
 gtgtctcaga cattgatgta ccttttccct gcctcgctcc aggttttagt gaagtaaaca 850
 gtatttggaag agtt 864

 <210> 146
 20 <211> 1527
 <212> DNA
 <213> Homo sapience
 <220>
 <221> CDS
 25 <222> (25)...(801)

 <400> 146
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 Met Ala Val Leu Ala Pro Leu Ile Ala
 30 1 5
 ctc gtg tat tcg gtg ccg cga ctt tca cga tgg ctc gcc caa cct tac 99
 Leu Val Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr
 10 15 20 25
 tac ctt ctg tcg gcc ctg ctc tct gct gcc ttc cta ctc gtg agg aaa 147
 35 Tyr Leu Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys

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	30	35	40	
	ctg ccg ccg ctc tgc cac ggt ctg ccc acc caa cgc gaa gac ggt aac			195
	Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn			
	45	50	55	
5	ccg tgt gac ttt gac tgg aga gaa gtg gag atc ctg atg ttt ctc agt			243
	Pro Cys Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser			
	60	65	70	
	gcc att gtg atg atg aag aac cgc aga tcc atg ttc ctg atg acg tgc			291
	Ala Ile Val Met Met Lys Asn Arg Arg Ser Met Phe Leu Met Thr Cys			
10	75	80	85	
	aaa ccc ccc cta tat atg ggc cct gag tat atc aag tac ttc aat gat			339
	Lys Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp			
	90	95	100	105
	aaa acc att gat gag gaa cta gaa cgg gac aag agg gtc act tgg att			387
15	Lys Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile			
	110	115	120	
	gtg gag ttc ttt gcc aat tgg tct aat gac tgc caa tca ttt gcc cct			435
	Val Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro			
	125	130	135	
20	atc tat gct gac ctc tcc ctt aaa tac aac tgt aca ggg cta aat ttt			483
	Ile Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe			
	140	145	150	
	ggg aag gtg gat gtt gga cgc tat act gat gtt agt acg cgg tac aaa			531
	Gly Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys			
25	155	160	165	
	gtg agc aca tca ccc ctc acc aag caa ctc cct acc ctg atc ctg ttc			579
	Val Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe			
	170	175	180	185
	caa ggt ggc aag gag gca atg cgg cgg cca cag att gac aag aaa gga			627
30	Gln Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly			
	190	195	200	
	cgg gct gtc tca tgg acc ttc tct gag gag aat gtg atc cga gaa ttt			675
	Arg Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe			
	205	210	215	
35	aac tta aat gag cta tac cag cgg gcc aag aaa cta tca aag gct gga			723

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Asn Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly
 220 225 230
 gac aat atc cct gag gag cag cct gtg gct tca acc ccc acc aca gtg 771
 Asp Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val
 5 235 240 245
 tca gat ggg gaa aac aag aag gat aaa taagatcctc ac 810
 Ser Asp Gly Glu Asn Lys Lys Asp Lys
 250 255
 tttggcagtg cttcctctcc tgtcaattcc aggcctcttc cataaccaca agcctgaggc 870
 10 tgcagccttt tatttatgtt ttccctttgg ctgtgactgg gtggggcagc atgcagcttc 930
 tgatttttaa gaggcata ggggaattgtc aggcacccta caggaaggcc tgccatgctg 990
 tggccaactg tttcactgga gcaagaaaga gatctcatag gacggagggg gaaatggttt 1050
 cctccaagc ttgggtcagt gtgttaactg cttatcagct attcagacat ctccatggtt 1110
 tctccatgaa actctgtggt ttcattcattc cttcttagtt gacctgcaca gcttggttag 1170
 15 acctagattt aaccctaagg taagatgctg gggatataga cgctaagaat tttcccccaa 1230
 ggactcttgc ttccttaagc cttctgtggt tcgtttatgg tcttcattaa aagtataagc 1290
 ctaactttgt cgctagtctt aaggagaaac ctttaaccac aaagttttta tcattgaaga 1350
 caatattgaa caacccccta ttttgtgggg attgagaagg ggtgaataga ggcttgagac 1410
 tttcctttgt gtggtaggac ttggaggaga aatcccctgg actttcacta accctctgac 1470
 20 atactcccca caccagttg atggctttcc gtaataaaaa gattgggatt tcctttt 1527

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 aagtagtggt tccggcgccg tgttccagct ccggttggtt ccgcgagaaa gcgagaggcc 120
 gagcccgggc tgggtgcg atg gcc gcg gtg gtg gcc aag cgg gaa ggg ccg 170
 Met Ala Ala Val Val Ala Lys Arg Glu Gly Pro
 35 1 5 10

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ccg ttc atc agc gag gcg gcc gtg cgg ggc aac gcc gcc gtc ctg gat 218
 Pro Phe Ile Ser Glu Ala Ala Val Arg Gly Asn Ala Ala Val Leu Asp
 15 20 25
 tat tgc cgg acc tcg gtg tca gcg ctg tcg ggg gcc acg gcc ggc atc 266
 5 Tyr Cys Arg Thr Ser Val Ser Ala Leu Ser Gly Ala Thr Ala Gly Ile
 30 35 40
 ctc ggc ctc acc ggc ctc tac ggc ttc atc ttc tac ctg ctc gcc tcc 314
 Leu Gly Leu Thr Gly Leu Tyr Gly Phe Ile Phe Tyr Leu Leu Ala Ser
 45 50 55
 10 gtc ctg ctc tcc ctg ctc ctc att ctc aag gcg gga agg agg tgg aac 362
 Val Leu Leu Ser Leu Leu Leu Ile Leu Lys Ala Gly Arg Arg Trp Asn
 60 65 70 75
 aaa tat ttc aaa tca cgg aga cct ctc ttt aca gga ggc ctc atc ggg 410
 Lys Tyr Phe Lys Ser Arg Arg Pro Leu Phe Thr Gly Gly Leu Ile Gly
 15 80 85 90
 ggc ctc ttc acc tac gtc ctg ttc tgg acg ttc ctc tac ggc atg gtg 458
 Gly Leu Phe Thr Tyr Val Leu Phe Trp Thr Phe Leu Tyr Gly Met Val
 95 100 105
 cac gtc tac tgaaatgggg gcccggggga cttttttaaa aaa 500
 20 His Val Tyr
 110
 ccagatcggg aggactgtgg ccagcaatta acaccatgta gacttcetta gttettaagt 560
 ggttgaattc gctgcttgtt ctgtaacgtt ataaataatt tatatctgaa gacggagagc 620
 ctgtaatat cttcagatta aatgaagcgt gagacactt 659
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 <213> Homo sapience
 30 <220>
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 <222> (68)...(343)
 <400> 148
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 Met Val Tyr Ile Ser Asn Gly Gln Val Leu Asp Ser Arg Ser
 1 5 10
 5 cag tct cca tgg aga tta tct ttg ata aca gat ttc ttc tgg gga ata 157
 Gln Ser Pro Trp Arg Leu Ser Leu Ile Thr Asp Phe Phe Trp Gly Ile
 15 20 25 30
 gct gag ttt gtg gtt ttg ttt ttc aaa act ctg ctt cag caa gat gtg 205
 Ala Glu Phe Val Val Leu Phe Phe Lys Thr Leu Leu Gln Gln Asp Val
 35 40 45
 10 aaa aaa aga aga agc tat gga aac tca tct gat tcc aga tat gat gat 253
 Lys Lys Arg Arg Ser Tyr Gly Asn Ser Ser Asp Ser Arg Tyr Asp Asp
 50 55 60
 gga aga ggg cca cca gga aac cct ccc cga aga atg ggt aga atc aat 301
 Gly Arg Gly Pro Pro Gly Asn Pro Pro Arg Arg Met Gly Arg Ile Asn
 15 65 70 75
 cat ctg cgt ggc cct agt ccc cct cca atg gct ggt gga tgaggaaggt 350
 His Leu Arg Gly Pro Ser Pro Pro Pro Met Ala Gly Gly
 80 85 90
 20 aaatgtctgc tctaagaagc agacaaccgg acatgcgcat tcatagcaga aggaaaccat 410
 caagaagtgg aaggctgacc atgatgagca gtagatgaat gtgtatgtct aaacaaggac 470
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 cctgactgac atgcagttcc ataaatgcag atgtttgtct cattaccttt ttgtatagtt 590
 tattaaagta ttaatatagt ttaataaagt aaatatTTTT aggttgcaga atggactcct 650
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 <213> Homo sapience
 30 <220>
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 <400> 149
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	atg ttc acc agc acc ggc tcc agt ggg ctc tac aag gcg cct ctg tgc	103
	Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro Leu Ser	
	1 5 10 15	
5	aag agc ctt ctg ctg gtc ccc agt gcc ctc tcc ctc ctg ctc gcc ctc	151
	Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu Ala Leu	
	20 25 30	
	ctc ctg cct cac tgc cag aag ctc ttt gtg tat gac ctt cac gca gtc	199
	Leu Leu Pro His Cys Gln Lys Leu Phe Val Tyr Asp Leu His Ala Val	
	35 40 45	
10	aag aac gac ttc cag att tgg agg ttg ata tgt gga aga ata att tgc	247
	Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile Ile Cys	
	50 55 60	
	ctt gat ttg aaa gat act ttc tgc agt agt ctg ctt att tat aat ttt	295
	Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr Asn Phe	
15	65 70 75 80	
	agg ata ttt gaa aga aga tat gga agc aga aaa ttt gca tcc ttt ttg	343
	Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser Phe Leu	
	85 90 95	
	ctg ggt tcc tgg gtt ttg tca gcc tta ttt gac ttt ctc ctc att gaa	391
20	Leu Gly Ser Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu Ile Glu	
	100 105 110	
	gct atg cag tat ttc ttt ggc atc act gca gct agt aat ttg cct tct	439
	Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu Pro Ser	
	115 120 125	
25	gga ttc ctg gca cct gtg ttt gct ctg ttt gta cca ttt tac tgc tcc	487
	Gly Phe Leu Ala Pro Val Phe Ala Leu Phe Val Pro Phe Tyr Cys Ser	
	130 135 140	
	ata cca aga gtc caa gtg gca caa att ctg ggt ccg ttg tcc atc aca	535
	Ile Pro Arg Val Gln Val Ala Gln Ile Leu Gly Pro Leu Ser Ile Thr	
30	145 150 155 160	
	aac aag aca ttg att tat ata ttg gga ctg cag ctt ttc acc tct ggt	583
	Asn Lys Thr Leu Ile Tyr Ile Leu Gly Leu Gln Leu Phe Thr Ser Gly	
	165 170 175	
	tcc tac atc tgg att gta gcc ata agt gga ctt atg tcc ggt ctg tgc	631
35	Ser Tyr Ile Trp Ile Val Ala Ile Ser Gly Leu Met Ser Gly Leu Cys	

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	180	185	190	
	tac gac agc aaa atg ttc cag gtg cat cag gtg ctc tgc atc ccc agc	679		
	Tyr Asp Ser Lys Met Phe Gln Val His Gln Val Leu Cys Ile Pro Ser			
	195	200	205	
5	tgg atg gca aaa ttc ttt tct tgg aca ctt gaa ccc atc ttc tct tct	727		
	Trp Met Ala Lys Phe Phe Ser Trp Thr Leu Glu Pro Ile Phe Ser Ser			
	210	215	220	
	tca gaa ccc acc agc gaa gcc aga att ggg atg gga gcc acg ctg gac	775		
	Ser Glu Pro Thr Ser Glu Ala Arg Ile Gly Met Gly Ala Thr Leu Asp			
10	225	230	235	240
	atc cag aga cag cag aga atg gag ctg ctg gac cgg cag ctg atg ttc	823		
	Ile Gln Arg Gln Gln Arg Met Glu Leu Leu Asp Arg Gln Leu Met Phe			
	245	250	255	
	tct cag ttt gca caa ggg agg cga cag aga cag cag cag gga gga atg	871		
15	Ser Gln Phe Ala Gln Gly Arg Arg Gln Arg Gln Gln Gln Gly Gly Met			
	260	265	270	
	atc aat tgg aat cgt ctt ttt cct cct tta cgt cag cga caa aac gta	919		
	Ile Asn Trp Asn Arg Leu Phe Pro Pro Leu Arg Gln Arg Gln Asn Val			
	275	280	285	
20	aac tat cag ggc ggt cgg cag tct gag cca gca gcg ccc cct cta gaa	967		
	Asn Tyr Gln Gly Gly Arg Gln Ser Glu Pro Ala Ala Pro Pro Leu Glu			
	290	295	300	
	gtt tct gag gaa cag gtc gcc cgg ctc atg gag atg gga ttt tcc aga	1015		
	Val Ser Glu Glu Gln Val Ala Arg Leu Met Glu Met Gly Phe Ser Arg			
25	305	310	315	320
	ggt gat gct ttg gaa gcc ctg aga gct tca aac aat gac ctc aat gtc	1063		
	Gly Asp Ala Leu Glu Ala Leu Arg Ala Ser Asn Asn Asp Leu Asn Val			
	325	330	335	
	gcc acc aac ttc ctg ctg cag cac tgatagtccc aggccaacac tgg	1110		
30	Ala Thr Asn Phe Leu Leu Gln His			
	340			
	gaccggaccg gcagccgagt gacagtgcgt ggtecccacc atcagatcag cccggggacc	1170		
	gagcatctct ggtgctgatg ttcttgtggg aagagggagg ttccaccgca cccctgccet	1230		
	caaccgcaag actgttgccg ttttagtgtg gagataagtt tgccattaca ttagcatgta	1290		
35	ttttctatct atatttttta ttgggcattt tccctagggt ggagagtcag cactcgtttt	1350		

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	gaatgtgttt aaaatgcatt aaaatggaag atttctgcag gcagttgaat ggcactccag	1410
	atggggaatt gctgtaaccc tcttactgta acatgtcatc tcctgcgtcg tgatggggag	1470
	agggtaaatgt tacttcacaa aggacatgtc agatccttct tcatggactt ttttagttac	1530
	tgttttttct ctcaaacttg ttttcgaatc tcctgggagt gagggagaaa caggagactg	1590
5	aatcctcccc caagctgttc caggccagag gactctgcag taccttctcc tacatctagt	1650
	aacaaagaat ggtgataacc atgcactggg tcaaggttct ggagttctcc atgaaacttg	1710
	ggttaatttt gctcagagta tccggagtta gccactaggc tgcgggtgaa atgggatgga	1770
	gtagaacaac agcaggcttc ctggagccac atgggctgac tagggcactc tgtggctggc	1830
	ctggcacggg ctccagcccag gaagaggaga aacgatccct tgctgcccc tccctgtggc	1890
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	ctcagggtt ggggtcttcaa cctgtggcga caggaggcag ggcagactgt ggaggacagg	2010
	atgcaggtea gggagagggg aggcaggggg ggaccgccat gagcatgaaa agaccogaag	2070
	caagttgact cttgcaatgt gcaactgtta tggtctgcaa aatgagcaac gatgtatcaa	2130
	attgatgcaa atttagatgt tgatacttac aataaagttt ttaatgtgtt tt	2182
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	acgtgcctcc tggtcccgac gtagctcgca gctccccagt ctcactccat tccttcccca	120
	cctggcgcgc acctgctcaa gaccagggtc ctgccaaagc ctaggagggc gcgtgccagg	180
	ggcgtaggg aactgaggag cgcgcgcgcc atg ggg ccg ccg cct ggg gcc	231
	Met Gly Pro Pro Pro Gly Ala	
30	1 5	
	ggg gtc tcc tgc cgc ggt ggc tgc ggc ttt tcc aga ttg ctg gca tgg	279
	Gly Val Ser Cys Arg Gly Gly Cys Gly Phe Ser Arg Leu Leu Ala Trp	
	10 15 20	
	tgc ttc ctg ctg gcc ctg agt ccg cag gca ccc ggt tcc cgg ggg gct	327
35	Cys Phe Leu Leu Ala Leu Ser Pro Gln Ala Pro Gly Ser Arg Gly Ala	

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	25	30	35	
	gaa gca gtg tgg acc gcg tac ctc aac gtg tcc tgg cgg gtt ccg cac			375
	Glu Ala Val Trp Thr Ala Tyr Leu Asn Val Ser Trp Arg Val Pro His			
	40	45	50	55
5	acg gga gtg aac cgt acg gtg tgg gag ctg agc gag gag ggc gtg tac			423
	Thr Gly Val Asn Arg Thr Val Trp Glu Leu Ser Glu Glu Gly Val Tyr			
	60	65	70	
	ggc cag gac tgg ccg ctg gag cct gtg gct ggg gtc ctg gta ccg ccc			471
	Gly Gln Asp Ser Pro Leu Glu Pro Val Ala Gly Val Leu Val Pro Pro			
10	75	80	85	
	gac ggg ccc ggg gcg ctt aac gcc tgt aac ccg cac acg aat ttc acg			519
	Asp Gly Pro Gly Ala Leu Asn Ala Cys Asn Pro His Thr Asn Phe Thr			
	90	95	100	
	gtg ccc acg gtt tgg gga agc acc gtg caa gtc tct tgg ttg gcc ctc			567
15	Val Pro Thr Val Trp Gly Ser Thr Val Gln Val Ser Trp Leu Ala Leu			
	105	110	115	
	atc caa cgc ggc ggg ggc tgc acc ttc gca gac aag atc cat ctg gct			615
	Ile Gln Arg Gly Gly Gly Cys Thr Phe Ala Asp Lys Ile His Leu Ala			
	120	125	130	135
20	tat gag aga ggg gcg tct gga gcc gtc atc ttt aac ttc ccc ggg acc			663
	Tyr Glu Arg Gly Ala Ser Gly Ala Val Ile Phe Asn Phe Pro Gly Thr			
	140	145	150	
	cgc aat gag gtc atc ccc atg tct cac ccg ggt gca gta gac att gtt			711
	Arg Asn Glu Val Ile Pro Met Ser His Pro Gly Ala Val Asp Ile Val			
25	155	160	165	
	gca atc atg atc ggc aat ctg aaa ggc aca aaa att ctg caa tct att			759
	Ala Ile Met Ile Gly Asn Leu Lys Gly Thr Lys Ile Leu Gln Ser Ile			
	170	175	180	
	caa aga ggc ata caa gtg aca atg gtc ata gaa gta ggg aaa aaa cat			807
30	Gln Arg Gly Ile Gln Val Thr Met Val Ile Glu Val Gly Lys Lys His			
	185	190	195	
	ggc cct tgg gtg aat cac tat tca att ttt ttc gtt tct gtg tcc ttt			855
	Gly Pro Trp Val Asn His Tyr Ser Ile Phe Phe Val Ser Val Ser Phe			
	200	205	210	215
35	ttt att att acg gcg gca act gtg ggc tat ttt atc ttt tat tct gct			903

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	Phe Ile Ile Thr Ala Ala Thr Val Gly Tyr Phe Ile Phe Tyr Ser Ala	
	220 225 230	
	cga agg cta cgg aat gca aga gct caa agc agg aag cag agg caa tta	951
	Arg Arg Leu Arg Asn Ala Arg Ala Gln Ser Arg Lys Gln Arg Gln Leu	
5	235 240 245	
	aag gca gat gct aaa aaa gct att gga agg ctt caa cta cgc aca ctg	999
	Lys Ala Asp Ala Lys Lys Ala Ile Gly Arg Leu Gln Leu Arg Thr Leu	
	250 255 260	
	aaa caa gga gac aag gaa att ggc cct gat gga gat agt tgt gct gtg	1047
10	Lys Gln Gly Asp Lys Glu Ile Gly Pro Asp Gly Asp Ser Cys Ala Val	
	265 270 275	
	tgc att gaa ttg tat aaa cca aat gat ttg gta cgc atc tta acg tgc	1095
	Cys Ile Glu Leu Tyr Lys Pro Asn Asp Leu Val Arg Ile Leu Thr Cys	
	280 285 290 295	
15	aac cat att ttc cat aag aca tgt gtt gac cca tgg ctg tta gaa cac	1143
	Asn His Ile Phe His Lys Thr Cys Val Asp Pro Trp Leu Leu Glu His	
	300 305 310	
	agg act tgc ccc atg tgc aaa tgt gac ata ctc aaa gct ttg gga att	1191
	Arg Thr Cys Pro Met Cys Lys Cys Asp Ile Leu Lys Ala Leu Gly Ile	
20	315 320 325	
	gag gtg gat gtt gaa gat gga tca gtg tct tta caa gtc cct gta tcc	1239
	Glu Val Asp Val Glu Asp Gly Ser Val Ser Leu Gln Val Pro Val Ser	
	330 335 340	
	aat gaa ata tct aat agt gcc tcc tcc cat gaa gag gat aat cgc agc	1287
25	Asn Glu Ile Ser Asn Ser Ala Ser Ser His Glu Glu Asp Asn Arg Ser	
	345 350 355	
	gag acc gca tca tct gga tat gct tca gta cag gga aca gat gaa ccg	1335
	Glu Thr Ala Ser Ser Gly Tyr Ala Ser Val Gln Gly Thr Asp Glu Pro	
	360 365 370 375	
30	cct ctg gag gaa cac gtg cag tca aca aat gaa agt cta cag ctg gta	1383
	Pro Leu Glu Glu His Val Gln Ser Thr Asn Glu Ser Leu Gln Leu Val	
	380 385 390	
	aac cat gaa gca aat tct gtg gca gtg gat gtt att cct cat gtt gac	1431
	Asn His Glu Ala Asn Ser Val Ala Val Asp Val Ile Pro His Val Asp	
35	395 400 405	

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	aac cca acc ttt gaa gaa gac gaa act cct aat caa gag act gct gtt	1479
	Asn Pro Thr Phe Glu Glu Asp Glu Thr Pro Asn Gln Glu Thr Ala Val	
	410 415 420	
	cga gaa att aaa tct taaaatctgt gtaaatagaa aacttgaacc attagt	1530
5	Arg Glu Ile Lys Ser	
	425	
	aataacagaa ctgccaatca gggcctagtt tctattaata aattggataa atttaataaa	1590
	ataagagtga tactgaaagt gctcagatga ctaatattat gctatagtta aatggcttaa	1650
	aatattttaac ctgttaactt tttccacaa actcattata atatttttca taggcaagtt	1710
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	ttttcattta taacaatttt cttataaaaa catgttgctt ttaaaatgtg gagtagctgt	1830
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	tgcaaaactta ggcgagtact tcttgaaatg tctatttaag ctgctttaag ttaatagaaa	2010
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	ggggggagaa ttccagggtgc cttaatataa agtttgaagc ttcattccacc aaagttaa	2550
	agagctatct aaaaatgcac tttatttgta ctctgtgtgg cttttgtttt agaattttgt	2610
25	tcaaattata gcagaattta ggcaaaaata aaacagacat gtatttttgt ttgctgaatg	2670
	gatgaaacca ttgcattctt gtacactgat ttgaaatgct gtaaataatgt cccaatttgt	2730
	attgattctc tttaaatata aaatgtaa	2773